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(54) **VIALE GRAM NEGATIVE BACTERIA
LACKING OUTER MEMBRANE AGONISTS
OF TLR4/MD-2**

(75) Inventors: **David Bramhill**, Tucson, AZ (US); **Uwe Mamat**, Schleswig-Holstein (DE)

(73) Assignee: **RESEARCH CORPORATION
TECHNOLOGIES, INC.**, Tucson, AZ
(US)

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C12N 15/70 (2006.01)
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C12N 15/78 (2006.01)
C12P 19/34 (2006.01)
C12P 21/02 (2006.01)
C40B 40/02 (2006.01)

(52) **U.S. Cl.**

CPC **C12N 15/70** (2013.01); **C12N 15/1037**
(2013.01); **C12N 15/78** (2013.01); **C12P 19/34**
(2013.01); **C12P 21/02** (2013.01); **C40B 40/02**
(2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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Primary Examiner — Jennifer Graser

(74) Attorney, Agent, or Firm — Scully, Scott, Murphy & Presser, P.C.

(57) **ABSTRACT**

Viable Gram-negative bacteria or components thereof comprising outer membranes that substantially lack a ligand, such as Lipid A or 6-acyl lipidpolysaccharide, that acts as an agonist of TLR4/MD2. The bacteria may comprise reduced activity of arabinose-5-phosphate isomerases and one or more suppressor mutations, for example in a transporter thereby increasing the transporters capacity to transport Lipid IVA or in membrane protein YhjD. One or more genes (e.g., lpxL, lpxM, pagP, lpxP, and/or eptA) may be substantially deleted and/or one or more enzymes (e.g., lpxL, lpxM, pagP, lpxP, and/or EptA) may be substantially inactive. The bacteria may be competent to take up extracellular DNA, may be donor bacteria, or may be members of a library. The present invention also features methods of creating and utilizing such bacteria.

23 Claims, 105 Drawing Sheets

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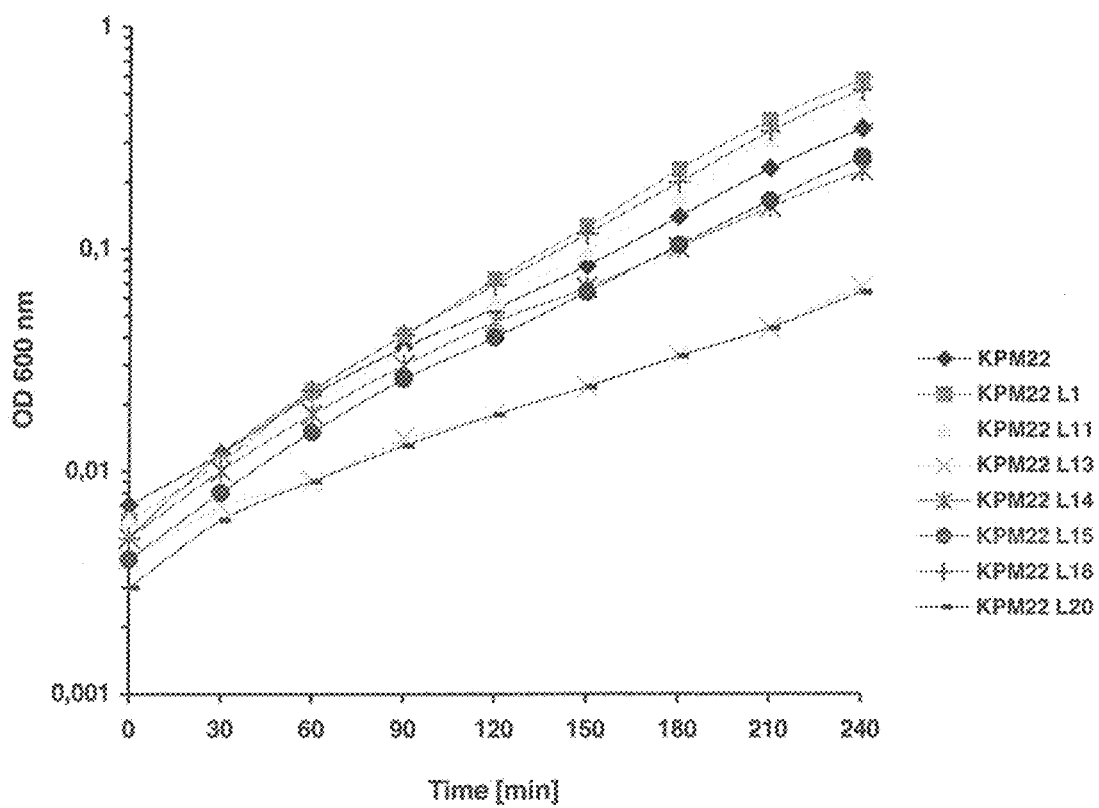


FIG. 1

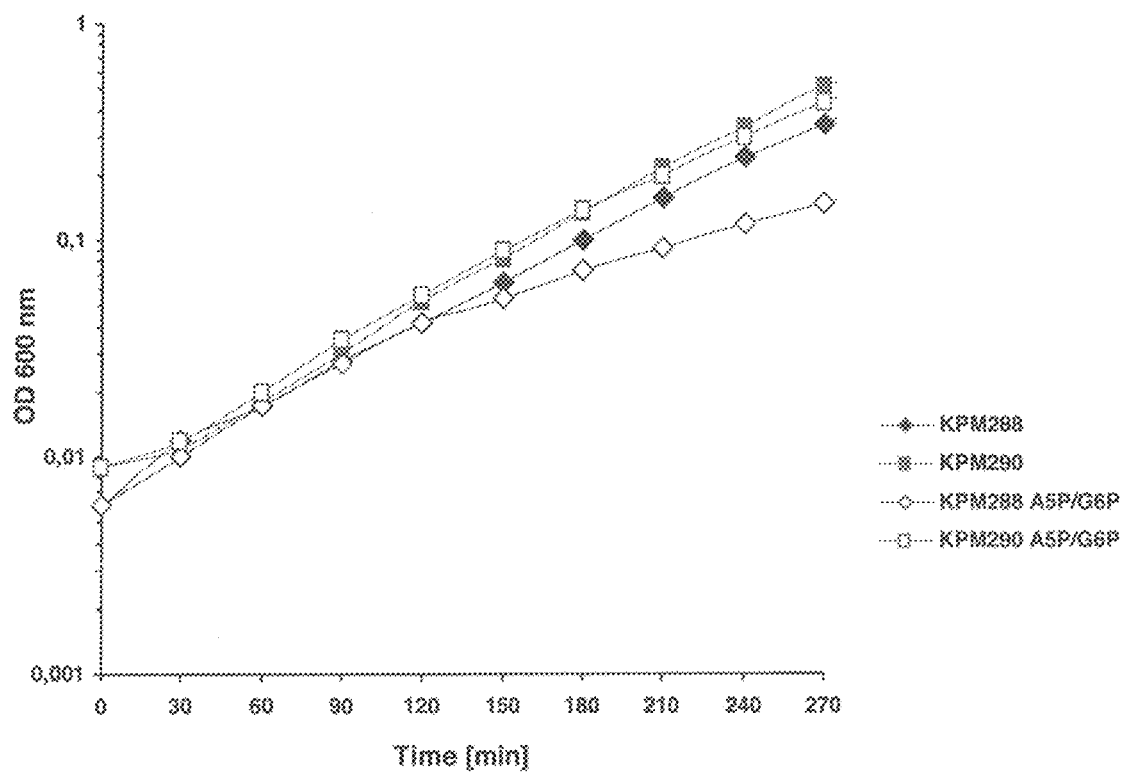


FIG. 2

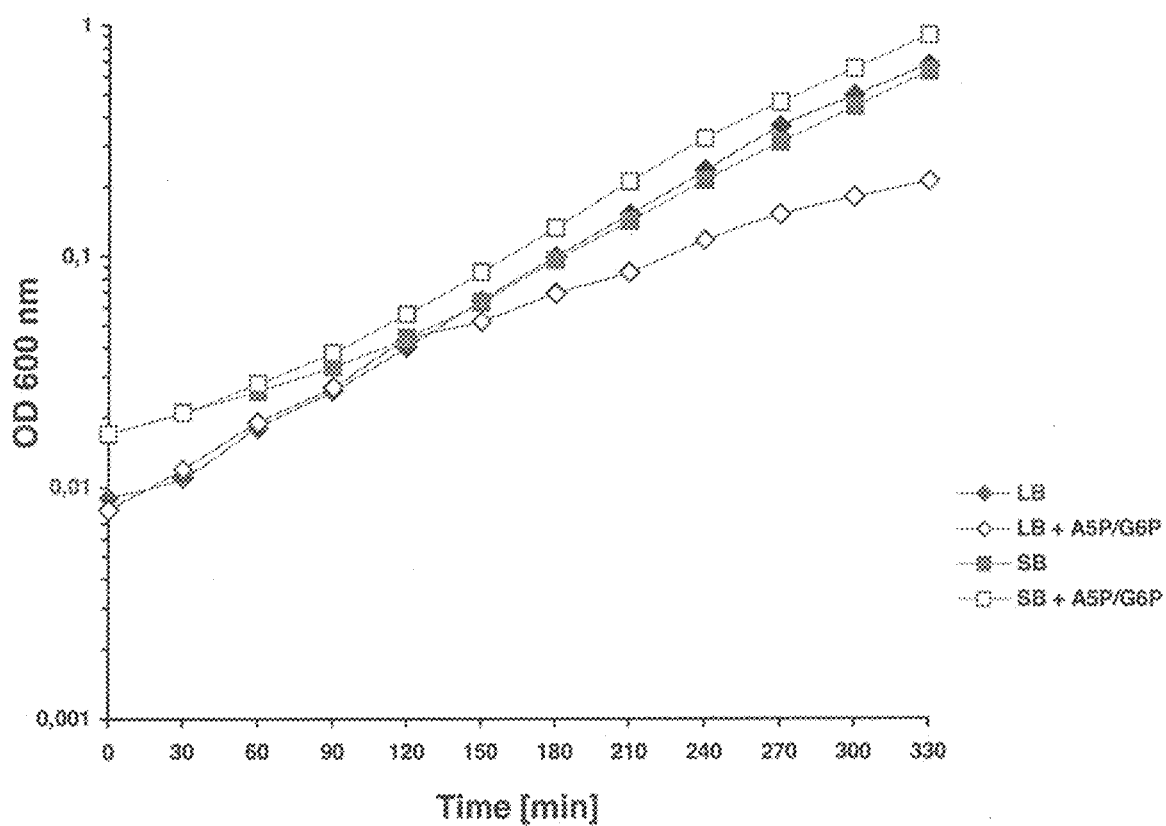


FIG. 3

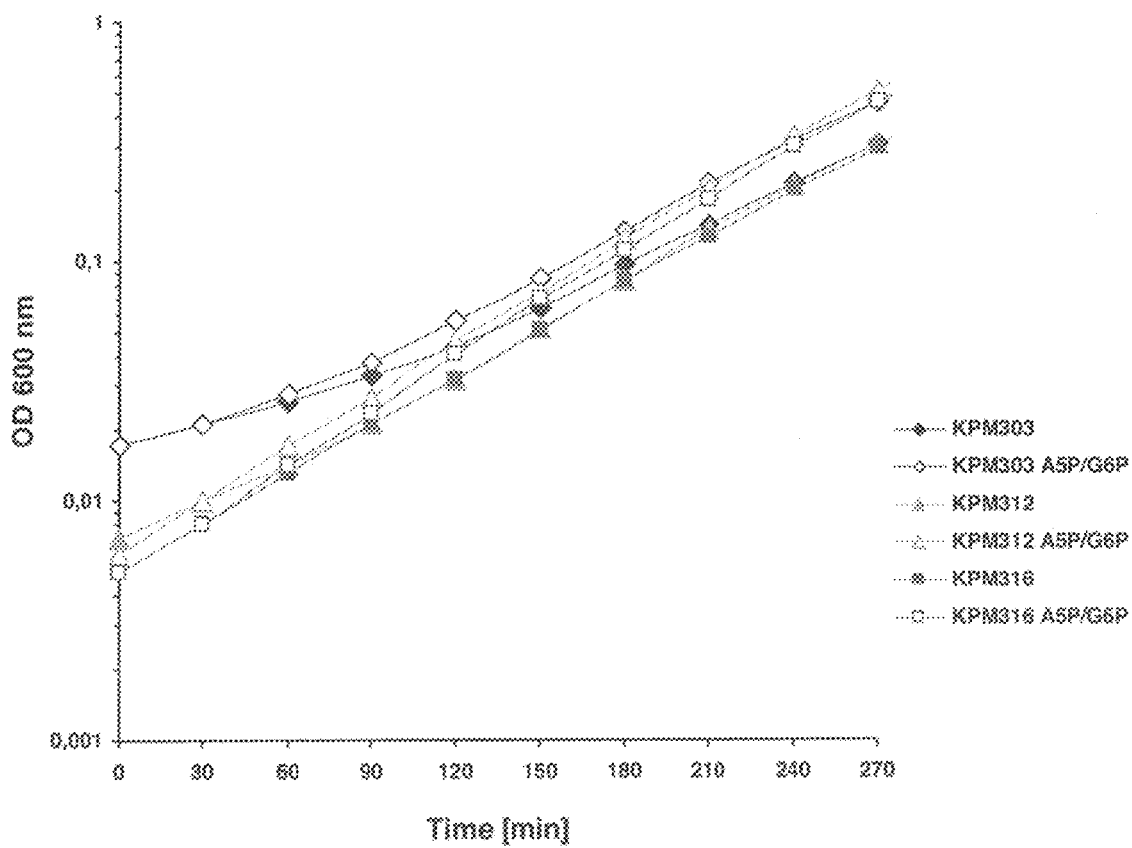


FIG. 4

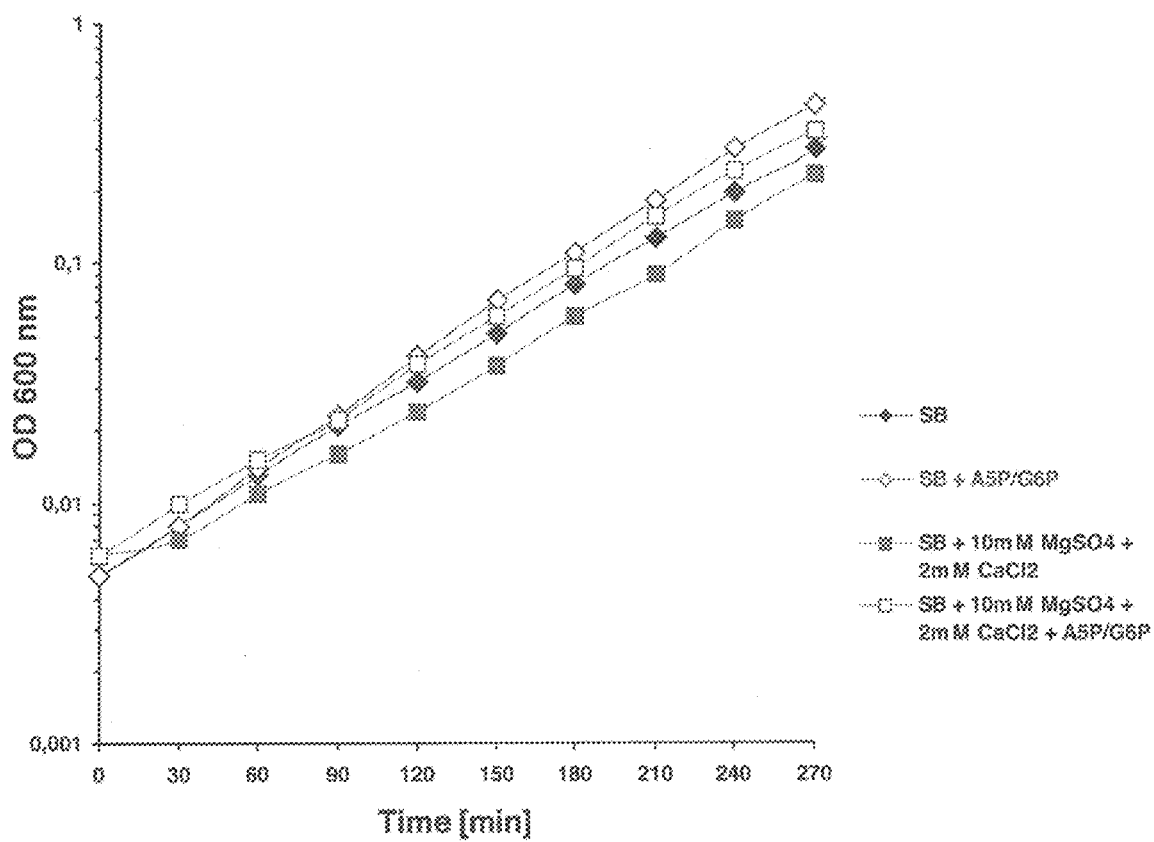
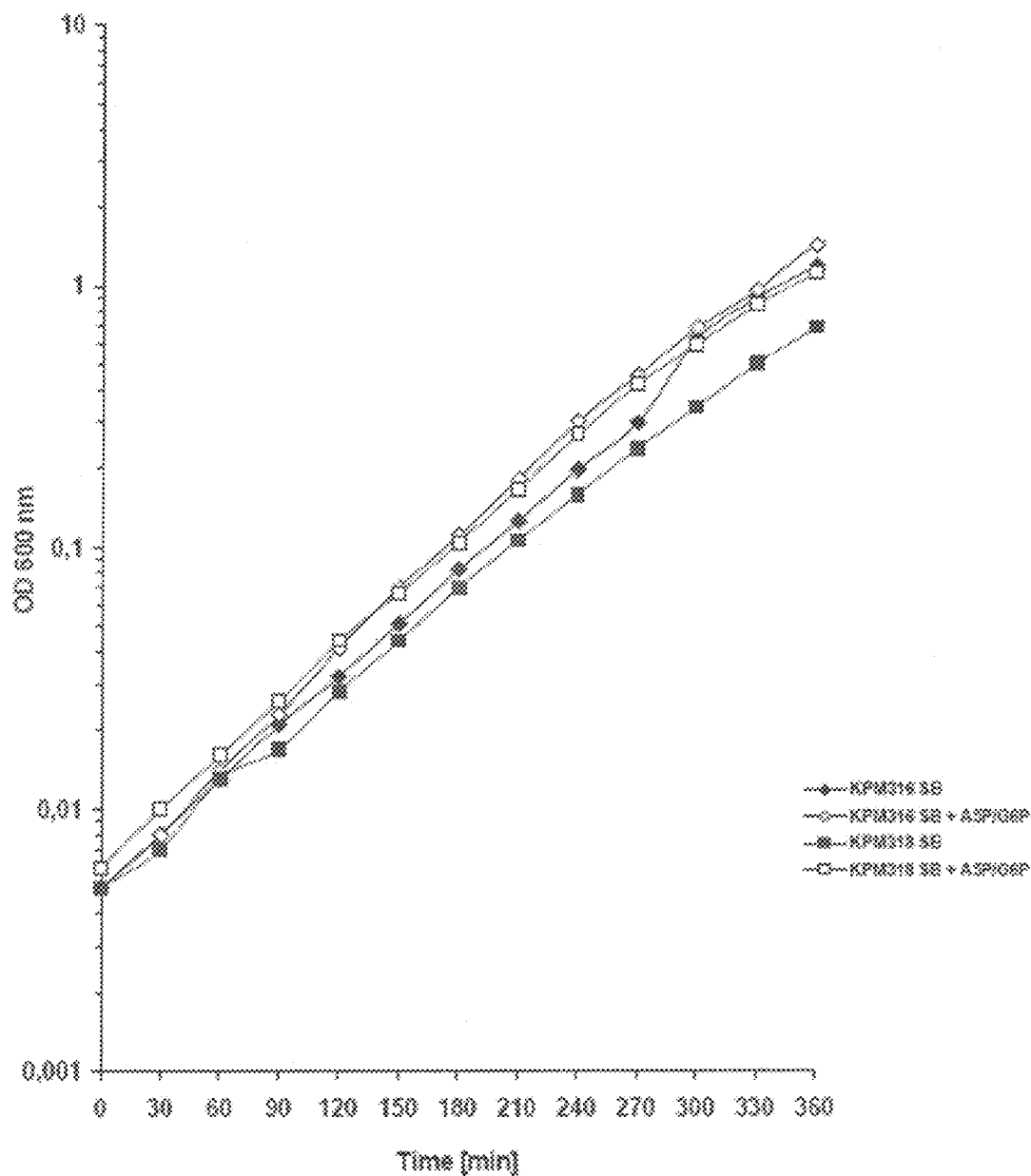


FIG. 5

FIG 6. Growth at 37 C of KPM316 and KPM318 in Super Broth with and without supplementation with arabinose-5-phosphate. Inset defines the symbols used for each strain and condition of growth.



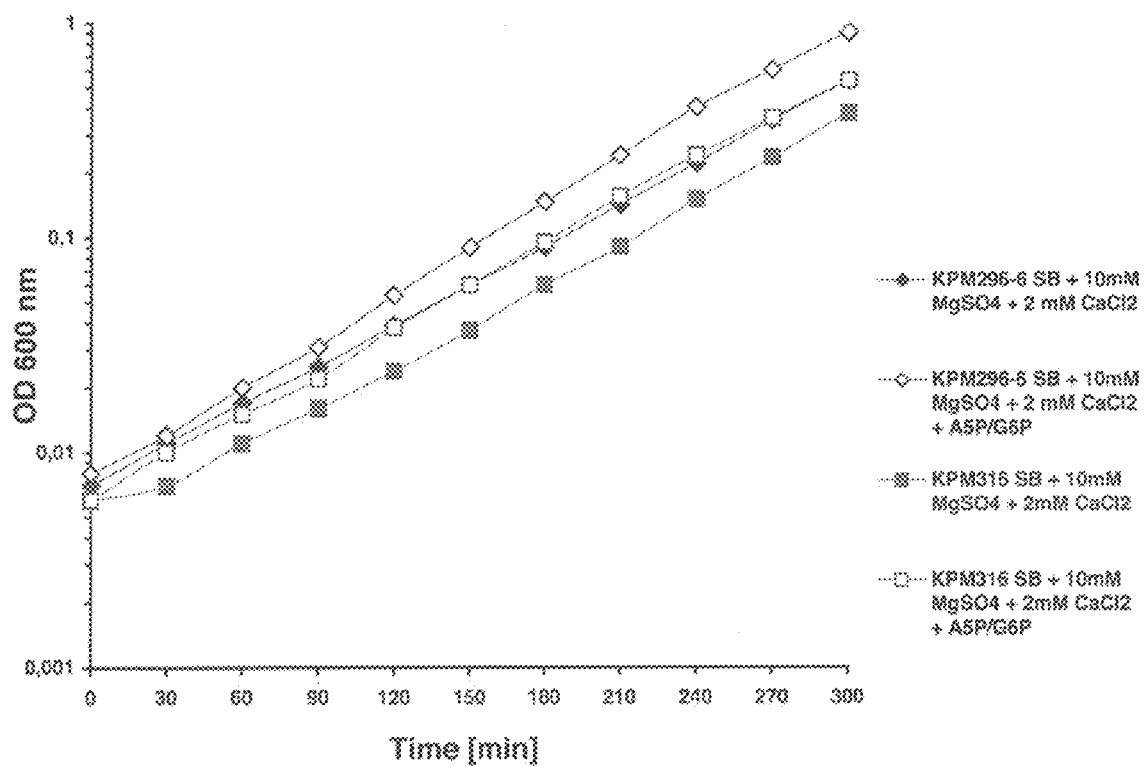


FIG. 7

FIG. 8

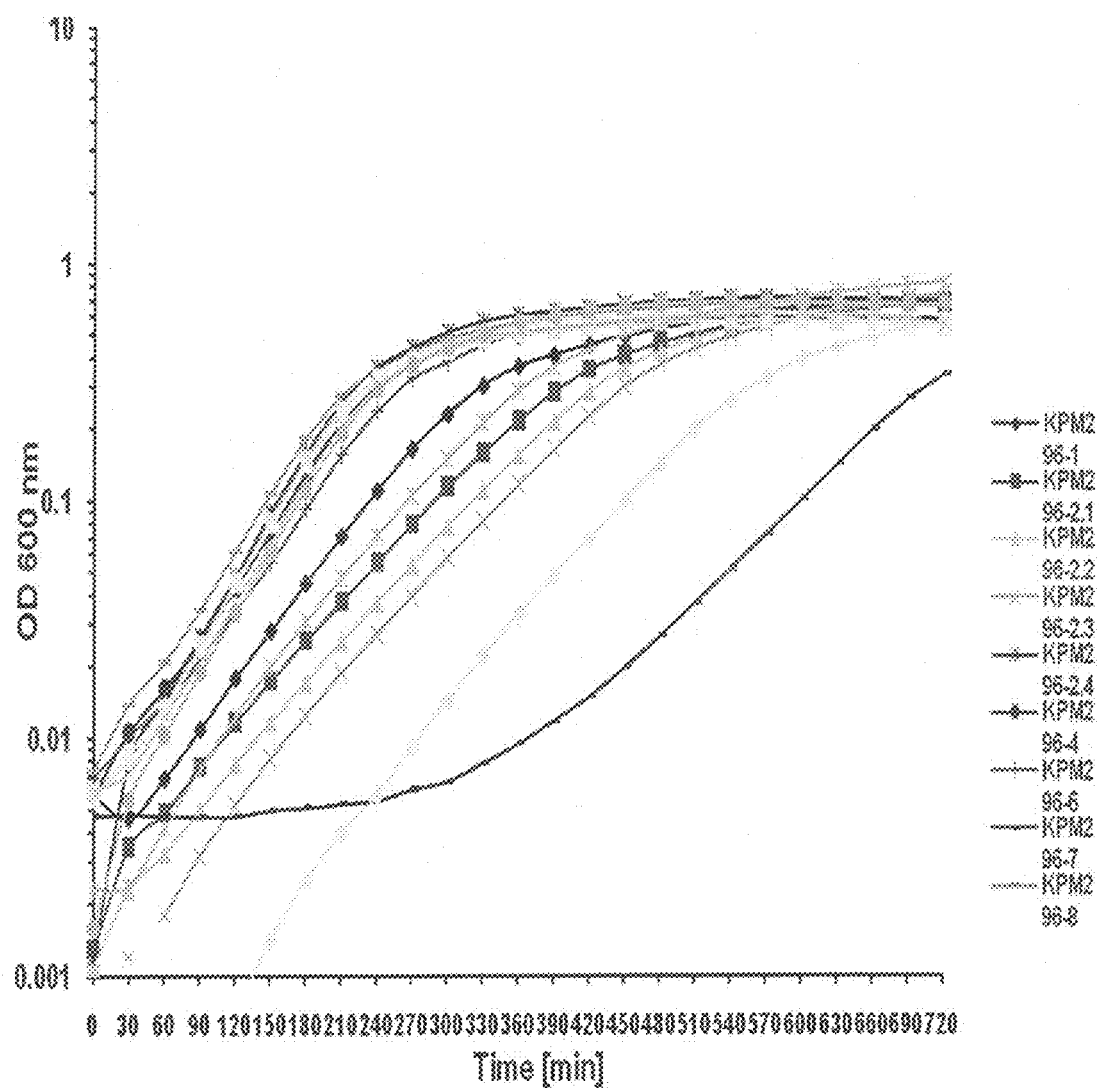
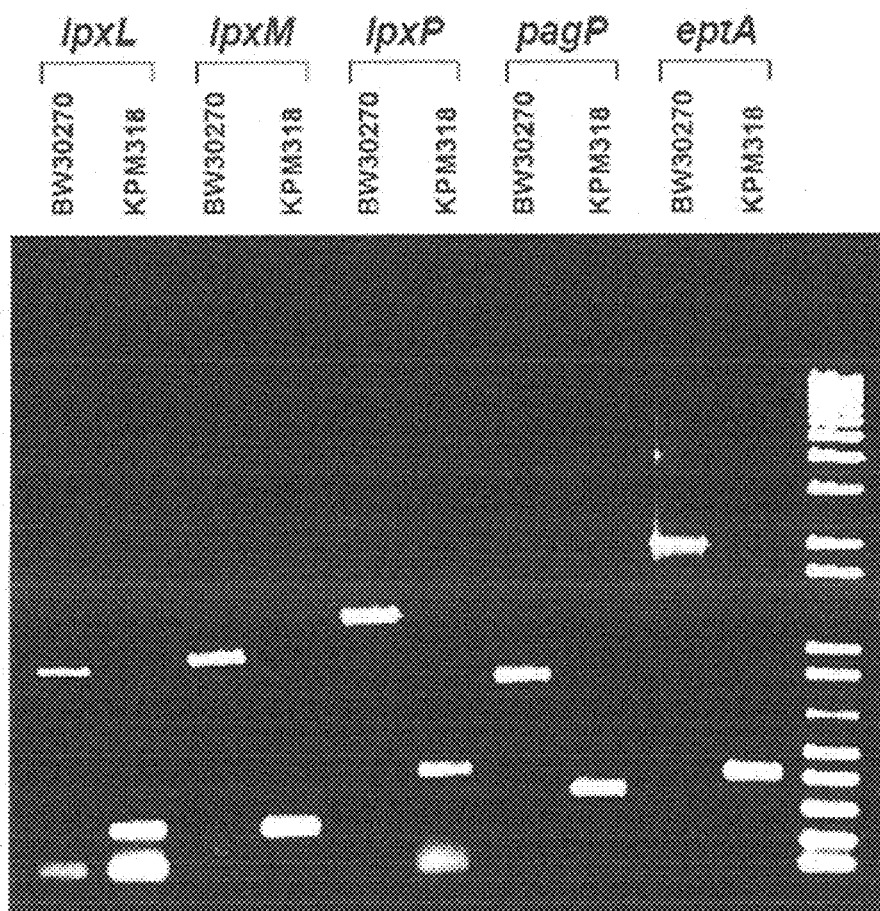


FIG. 9 PCR products generated from primer pairs flanking each of the genes deleted from KPM318 analysed by agarose gel electrophoresis and compared beside control PCR products from the parental strain BW30270.



HEK blue cell based assays of outer membranes from KPM316, KPM318 and BW30270 each grown in LB medium at 37 C.

(A) Outer membrane extracts of indicated strains from 2 microgramms down to 2 picogramms. Reference E. coli K12 LPS supplied in the kit is also shown.

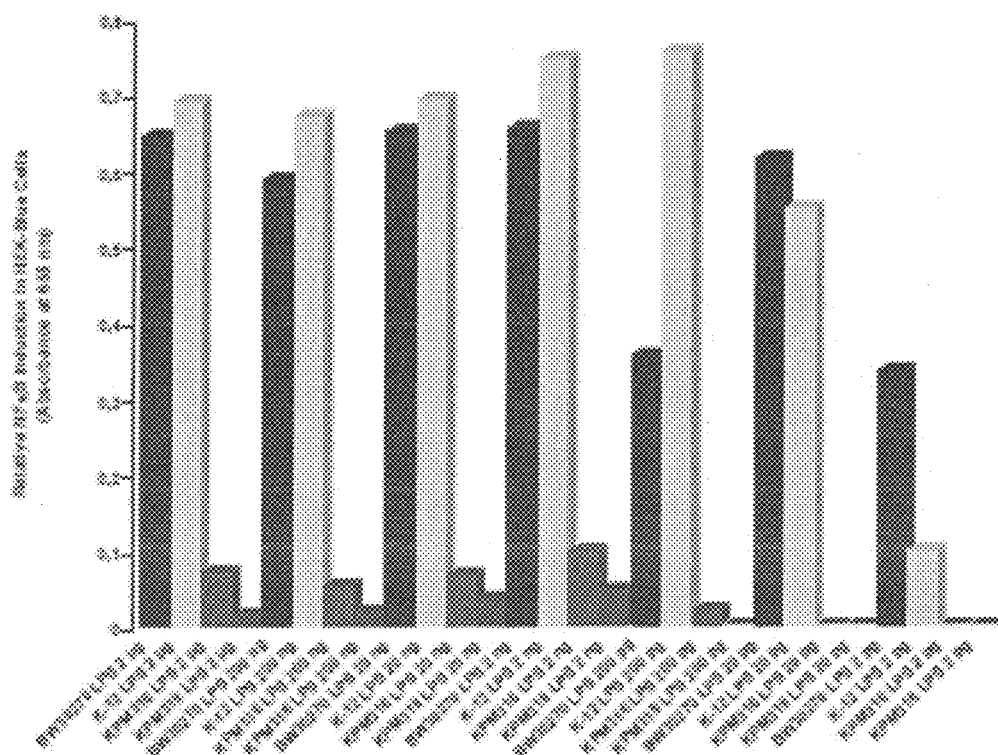


FIG. 10a

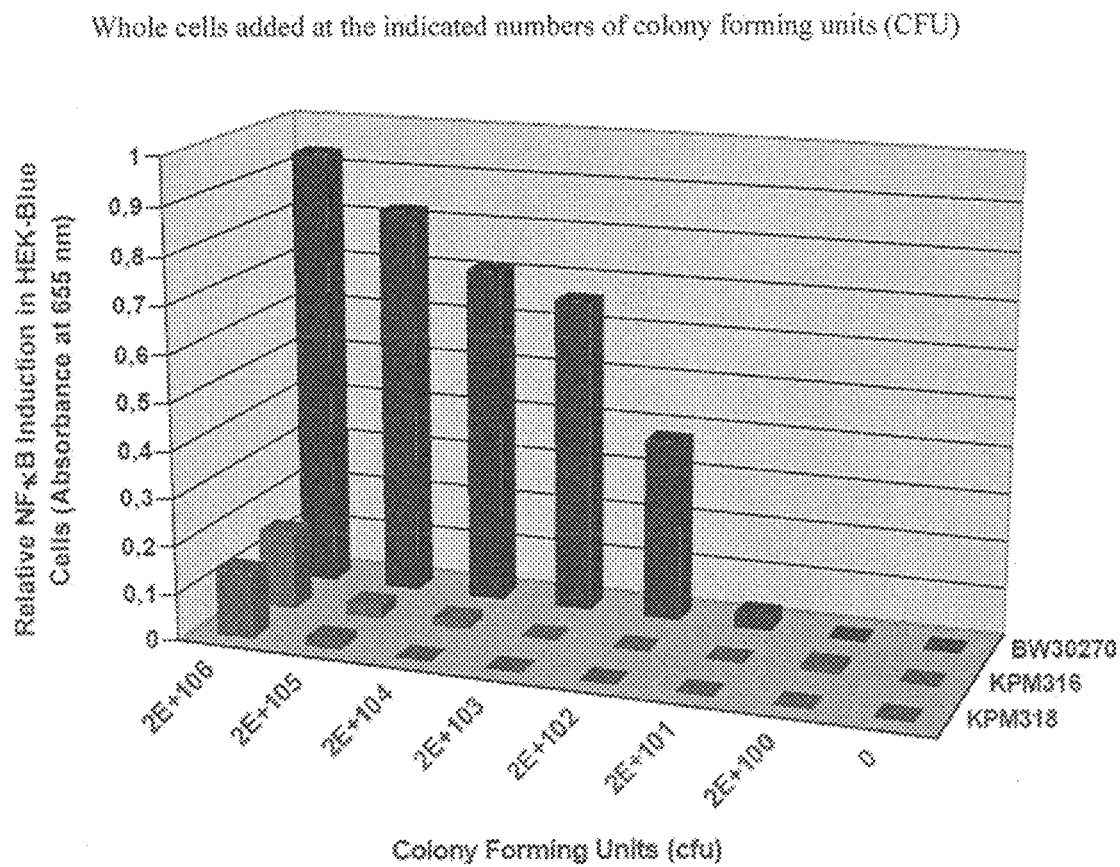
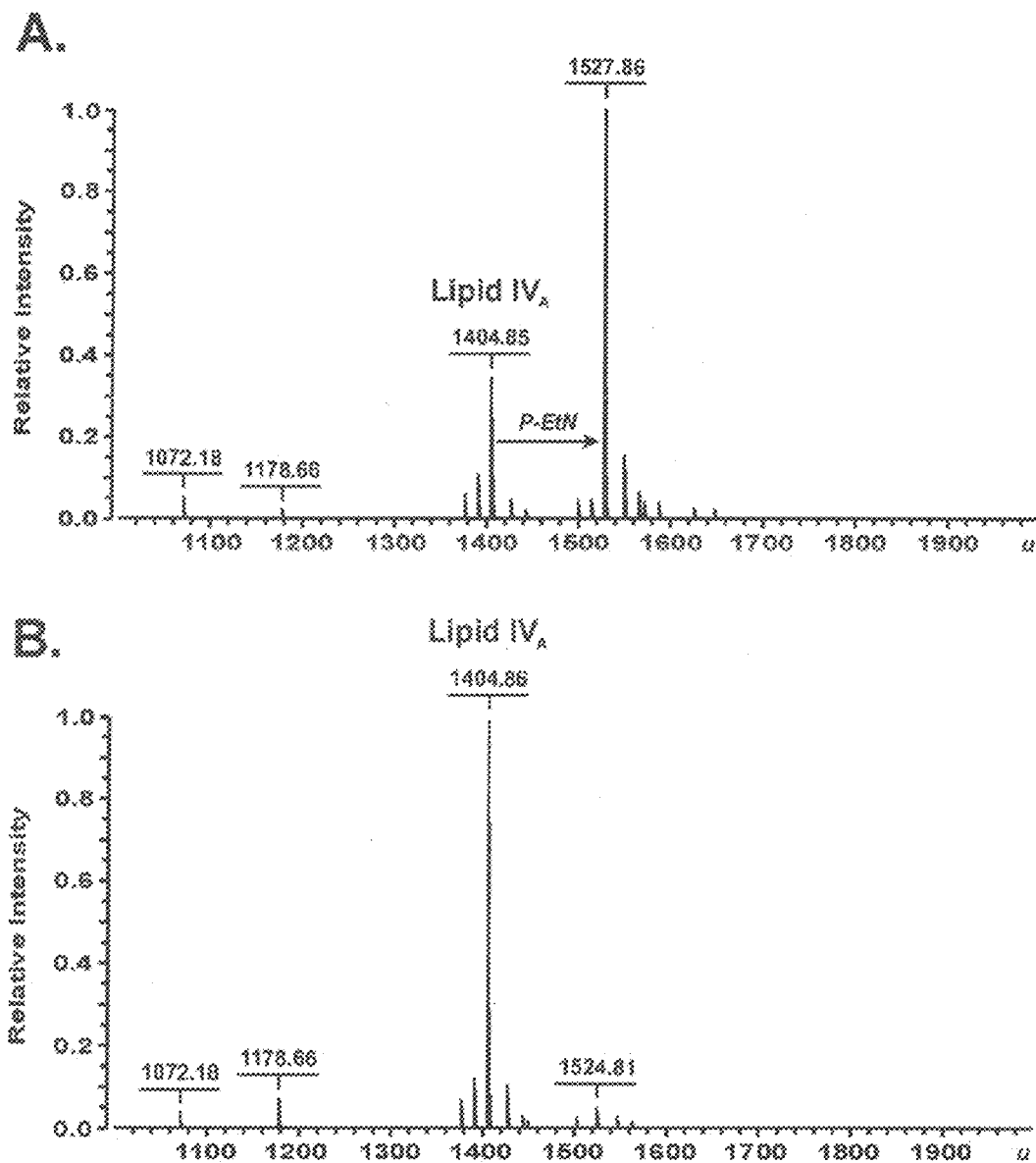


FIG. 10b

Figure 11. ESI-MS spectra of the outer membrane samples extracted from KPM316 (A) and KPM318 (B).



Escherichia coli KPM316 (*msbA52* Δ *kdsD* Δ *gutQ* Δ *lpxL* Δ *lpxM* Δ *pagP* Δ *lpxP*)

The sequence of the sense strand of the organism is the *E coli* reference sequence with the following alterations:

msbA52 replaces the wild type allele of *msbA*, wherein a C at 965895 is replaced by a T, resulting in a Serine instead of Proline at amino acid 18 in the MsbA protein.

SEQID9:

965844

C>T 965895

ATGCATAACGACAAAGATCTCTCTACGTGGCAGACATTCCGCCGACTGTGGTCAACCATTGC
GCCTTTCAAAGCGGGTCTGATCGTGGCGGGCGTAGCGTTAATCCTCAACGCAGCCAGCGAT
ACCTTCATGTTATCGCTCCTTAAGCCACTTCTTGATGATGGCTTTGGTAAACAGATCGCTCC
GTGCTGGTGTGGATGCCGCTGGTGGTATCGGGCTGATGATTTACGTGGTATCACCAGCT
ATGTCTCCAGCTACTGTATCTCCTGGGTATCAGGAAAGGTGGTAATGACCATGCGTCGCCG
CCTGTTTGGTCACATGATGGGAATGCCAGTTTCATTCTTTGACAAACAGTCAACGGGTACGC
TGTTGTACGTATTACCTACGATTCCGAACAGGTTGCTTCTTCTTCCGGCGCACTGATTA
CTGTTGTGCGTGAAGGTGCGTCGATCATCGGCCTGTTTCATCATGATGTTCTATTACAGTTGG
CAACTGTCGATCATTTTGATTGTGCTGGCACCATTGTTTCGATTGCGATTGCGTTGTATCG
AAGCGTTTTTCGCAACATCAGTAAAAACATGCAGAACACCATGGGGCAGGTGACCACCAGCG
CAGAACAAATGCTGAAGGGCCACAAAGAAGTATTGATTTTCGGTGGTCAGGAAGTGAAAC
GAAACGCTTTGATAAAGTCAGCAACCGAATGCGTCTTCAGGGGATGAAAATGGTTTCAGCCT
CTTCCATCTCTGATCCGATCATTACGCTGATCGCCTCTTTGGCGCTGGCGTTTGTCTGTAT
GCGGCGAGCTTCCCAAGTGTATGGATAGCCTGACTGCCGGTACGATTACCGTTGTTTTCTC
TTCAATGATTGCACTGATGCGTCCGCTGAAATCGCTGACCAACGTTAACGCCCAGTTCCAGC
GCGGTATGGCGGCTTGTGAGACGCTGTTTACCATTCTGGACAGTGAGCAGGAGAAAGATGA
AGGTAAGCGCGTGATCGAGCGTGGCAGCTGGCGACGTGGAATTCGCAATGTCACCTTTACT
TATCCGGGACGTGACGTACCTGCATTGCGTAACATCAACCTGAAAATTCCGGCAGGGAAGA
CGGTTGCTCTGGTTGGACGCTCTGGTTCGGGTAAATCAACCATCGCCAGCCTGATCACGCG
TTTTTACGATATTGATGAAGGCGAAATCCTGATGGATGGTCACGATCTGCGCGAGTATACCC
TGGCGTCGTTACGTAACCAGGTTGCTCTGGTGTGCGAGAATGTCCATCTGTTTAACGATACG
GTTGCTAACAAACATTGCTTACGCACGGACTGAACAGTACAGCCGTGAGCAAATTGAAGAAGC
GGCGCGTATGGCCTACGCCATGGACTTCATCAATAAGATGGATAACGGTCTCGATACAGTG
ATTGGTGAAAACGGCGTGCTGCTCTCTGGCGGTGAGCGTCAGCGTATTGCTATCGCTCGAG
CCTTGTTGCGTGATAGCCCGATTCTGATTCTGGACGAAGCTACCTCGGCTCTGGATACCGAA
TCCGAACGTGCGATTACGGCGGCACTGGATGAGTTGCAGAAAAACCGTACCTCTCTGGTGA
TTGCCACCGCTTGTCTACCATTGAAAAGGCAGACGAAATCGTGGTCGTCGAGGATGGTGT
CATTGTGGAACGCGGTACGCATAACGATTTGCTTGAGCACCGCGGCGTTTACGCGCAACTT
CACAAAATGCAGTTTGGCCAATGA

967592

FIG. 12a

ΔgutQ

Nucleotides 2827846 to 2828789 are deleted from the reference sequence and the following sequence is incorporated into KPM316 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM316 and correspond to bases of the MG1655 genome: C at 2827845 and G at 2828790):

SEQID10:

2827845

CGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAAGGTCGACGGATCCCCGGAATG

2828790

FIG. 12b

ΔkdsD

Nucleotides 3339288 to 3340264 are deleted from the reference sequence and the following sequence is incorporated into KPM316 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM316 and correspond to bases of the MG1655 genome: T at 3339287 and C at 3340265):

SEQID11:

3339287

TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAACTAAGGAGGATATTCATATGC

3340265

FIG. 12c

$\Delta lpxL$

(coding sequence of *lpxL* is complement of the reference nucleic acid strand)

Nucleotides 1114958 to 11155744 are deleted from the reference sequence and the following sequence is incorporated into KPM316 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM316 and correspond to bases of the MG1655 genome: C at 1114957 and C at 1115745):

SEQID12:

1114957

CTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTA
TAGGAACTTCGAAGCAGCTCCAGCCTACACC

1115745

FIG. 12d

 $\Delta lpxM$

(coding sequence of *lpxM* is complement of the reference nucleic acid strand)

Nucleotides 1937303 to 1938151 are deleted from the reference sequence and the following sequence is incorporated into KPM316 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM316 and correspond to bases of the MG1655 genome: G at 1937302 and G at 1938152):

SEQID13:

1937302

GTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTA
TAGGAACTTCGAAGCAGCTCCAGCCTACACG

1938152

FIG. 12e

ΔpagP

Nucleotides 655780 to 656340 are deleted from the reference sequence and the following sequence is incorporated into KPM316 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM316 and correspond to bases of the MG1655 genome: A at 655779 and G at 656341):

SEQID14:

655779

AGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAACTAAGGAGGATATTCATATGG

656341

FIG. 12f

ΔpxP

Nucleotides 2493667 to 2494587 are deleted from the reference sequence and the following sequence is incorporated into KPM316 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM316 and correspond to bases of the MG1655 genome: T at 2493666 and C at 2494588):

SEQID15:

2493666

TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAACTAAGGAGGATATTCATATGC

2494588

FIG. 12g

Reference Base Position (MG1655 ref)	Base in MG1655	Base in KPM316	Gene Affected	Predicted effect
547694	A	G	<i>ylbB</i>	E to E (silent)
3188791	C	T	<i>yqil</i>	S to S (silent)
3753464	G	C	<i>aldB</i>	T to T (silent)
3957957	C	T	No annotated feature in region	Unknown effect

FIG. 13

Escherichia coli KPM318 (*msbA52* Δ *kdsD* Δ *gutQ* Δ *lpxL* Δ *lpxM* Δ *pagP* Δ *lpxP* Δ *eptA*)

The sequence of the sense strand of the organism is the *E coli* reference sequence with the following alterations:

msbA52 replaces the wild type allele of *msbA*, wherein a C at 965895 is replaced by a T, resulting in a Serine instead of Proline at amino acid 18 in the MsbA protein.

SEQID16:

965844

C>T 965895

```
ATGCATAACGACAAAGATCTCTCTACGTGGCAGACATTCCGCCGACTGTGGTCAACCATTGC
GCCTTTCAAAGCGGGTCTGATCGTGGCGGGCGTAGCGTTAATCCTCAACGCAGCCAGCGAT
ACCTTCATGTTATCGCTCCTTAAGCCACTTCTTGATGATGGCTTTGGTAAAACAGATCGCTCC
GTGCTGGTGTGGATGCCGCTGGTGGTATCGGGCTGATGATTTTACGTGGTATCACCAGCT
ATGTCTCCAGCTACTGTATCTCCTGGGTATCAGGAAAGGTGGTAATGACCATGCGTCGCCG
CCTGTTTGGTCACATGATGGGAATGCCAGTTTCATTCTTTGACAAACAGTCAACGGGTACGC
TGTGTGTCACGTATTACCTACGATTCCGAACAGGTTGCTTCTTCTTCTTCCGGCGCACTGATTA
CTGTTGTGCGTGAAGGTGCGTCGATCATCGGCCTGTTTCATCATGATGTTCTATTACAGTTGG
CAACTGTCGATCATTTTGATTGTGCTGGCACCATTGTTTCGATTGCGATTCCGCTTGTATCG
AAGCGTTTTCGCAACATCAGTAAAAACATGCAGAACACCATGGGGCAGGTGACCACCAGCG
CAGAACAAATGCTGAAGGGCCACAAAGAAGTATTGATTTTCGGTGGTCAGGAAGTGGAAC
GAAACGCTTTGATAAAGTCAGCAACCGAATGCGTCTTCAGGGGATGAAAATGGTTTCAGCCT
CTTCCATCTCTGATCCGATCATTACGCTGATCGCCTCTTTGGCGCTGGCGTTTGTCTGTAT
GCGGCGAGCTTCCCAAGTGTCATGGATAGCCTGACTGCCGGTACGATTACCGTTGTTTTCTC
TTCAATGATTGCACTGATGCGTCCGCTGAAATCGCTGACCAACGTTAACGCCAGTTCCAGC
GCGGTATGGCGGCTTGTCAGACGCTGTTTACCATTCTGGACAGTGAGCAGGAGAAAGATGA
AGGTAAGCGCGTGATCGAGCGTGCGACTGGCGACGTGGAATTCCGCAATGTCACCTTTACT
TATCCGGGACGTGACGTACCTGCATTGCGTAACATCAACCTGAAAATTCCGGCAGGGAAGA
CGTTTGCTCTGTTGGACGCTCTGGTTCCGGTAAATCAACCATCGCCAGCCTGATCACGCG
TTTTTACGATATTGATGAAGGCGAAATCCTGATGGATGGTCACGATCTGCGCGAGTATACCC
TGCGCTCGTTACGTAACCAGGTTGCTCTGGTGTGCGAGAATGTCCATCTGTTTAACGATACG
GTTGCTAACAAACATTGCTTACGCACGGACTGAACAGTACAGCCGTGAGCAAATTGAAGAAGC
GGCGCGTATGGCCTACGCCATGGACTTCATCAATAAGATGGATAACGGTCTCGATACAGTG
ATTGGTGAAAACGGCGTGCTGCTCTCTGGCGGTACGCGTCAGCGTATTGCTATCGCTCGAG
CCTTGTTGCGTGATAGCCCGATTCTGATTCTGGACGAAGCTACCTCGGCTCTGGATACCGAA
TCCGAACGTGCGATTACGGCGGCACTGGATGAGTTGCAGAAAAACCGTACCTCTCTGGTGA
TTGCCACCGCTTGTCTACCATGAAAAGGCAGACGAAATCGTGGTCGTGAGGATGGTGT
CATTGTGGAACGCGGTACGCATAACGATTTGCTTGAGCACCGCGGCGTTTACGCGCAACTT
CACAAAATGCAGTTTGGCCAATGA
```

967592

FIG. 14a

ΔgutQ

Nucleotides 2827846 to 2828789 are deleted from the reference sequence and the following sequence is incorporated into KPM318 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM318 and correspond to bases of the MG1655 genome: C at 2827845 and G at 2828790):

SEQID17:

2827845

CGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAAGGTCGACGGATCCCCGGAATG

2828790

FIG. 14b

ΔkdsD

Nucleotides 3339288 to 3340264 are deleted from the reference sequence and the following sequence is incorporated into KPM318 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM318 and correspond to bases of the MG1655 genome: T at 3339287 and C at 3340265):

SEQID18:

3339287

TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAACTAAGGAGGATATTCATATGC

3340265

FIG. 14c

$\Delta lpxL$

(coding sequence of *lpxL* is complement of the reference nucleic acid strand)

Nucleotides 1114958 to 11155744 are deleted from the reference sequence and the following sequence is incorporated into KPM318 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM318 and correspond to bases of the MG1655 genome: C at 1114957 and C at 1115745):

SEQID19:

1114957

CTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTA
TAGGAACTTCGAAGCAGCTCCAGCCTACACC

1115745

FIG. 14d

$\Delta lpxM$

(coding sequence of *lpxM* is complement of the reference nucleic acid strand)

Nucleotides 1937303 to 1938151 are deleted from the reference sequence and the following sequence is incorporated into KPM318 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM318 and correspond to bases of the MG1655 genome: G at 1937302 and G at 1938152):

SEQID20:

1937302

GTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTA
TAGGAACTTCGAAGCAGCTCCAGCCTACACG

1938152

FIG. 14e

ΔpagP

Nucleotides 655780 to 656340 are deleted from the reference sequence and the following sequence is incorporated into KPM318 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM318 and correspond to bases of the MG1655 genome: A at 655779 and G at 656341):

SEQID21:

655779

AGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAACTAAGGAGGATATTCATATGG

656341

FIG. 14f

ΔpxP

Nucleotides 2493667 to 2494587 are deleted from the reference sequence and the following sequence is incorporated into KPM318 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM318 and correspond to bases of the MG1655 genome: T at 2493666 and C at 2494588):

SEQID22:

2493666

TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAAC
TTCGGAATAGGAACTAAGGAGGATATTCATATGC

2494588

FIG. 14g

ΔeptA

(coding sequence is complement of the reference nucleic acid strand)

Nucleotides 4331974 to 4333613 are deleted from the reference sequence and the following sequence is incorporated into KPM318 (the terminal nucleotides, shown at the ends of the sequence, are present in KPM318 and correspond to bases of the MG1655 genome: T at 4331973 and C at 4333614):

SEQID23:

4331973

TCATATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAG
TATAGGAACTTCGAAGCAGCTCCAGCCTACACC

4333614

FIG. 14h

BW30270**SNP Calls**

Ref Position	Consens. position	Ref. Allele	Mut. Allele	Freq	#	tot #	Gene	Amino acid change	Effect	Difference from MG1655
		Base	Base							
547694	532112	A	G	100	16	16	<i>ylbB</i>	E to E	silent	BW30270
3753464	3683218	G	C	100	22	22	<i>aldB</i>	T to T	silent	BW30270
3957957	3879611	C	T	100	9	9	none	?	no feature annotated	BW30270

DIP Calls

del/insertion cost=2/2

Ref Position	Consens. position	Ref. Allele	Mut. Allele	Freq	#	tot #	Gene	Change	Effect	
		Base	Base							
3558478	3490410	G	-	100	19	19	<i>glpR</i>	1 bp DEL	frameshift	BW30270

KPM318**SNP Calls**

Ref Position	Consens. position	Ref. Allele	Mut. Allele	Freq	#	tot #	Gene	Amino acid change	Effect	
		Base	Base							
547694	532113	A	G	100	17	17	<i>ylbB</i>	E to E	silent	BW30270
965895	941104	C	T	100	24	24	<i>msbA</i>	P18S	known suppressor	KPM96
3188791	3128701	C	T	100	18	18	<i>yqil</i>	S to S	silent	KPMs
3644838	3571752	G	T	100	15	15	<i>gor</i>	V173F	altered glutathione oxidoreductase activity??	KPMs
3753464	3678244	G	C	100	19	19	<i>aldB</i>	T to T	silent	BW30270
3798895	3720343	T	A	100	12	12	<i>rfaY</i>	T32Y	altered LPS core sugar synthesis??	KPMs
3957957	3874634	C	T	100	10	10	none	?	no feature annotated	BW30270

DIP Calls

del/insertion cost=2/2

Ref Position	Consens. position	Ref. Allele	Mut. Allele	Mutant Freq	#	tot #	Gene	Change	Effect	
		Base	Base							
3558478	3490410	G	-	100	18	18	<i>glpR</i>	1 bp DEL	frameshift	BW30270

FIG. 15

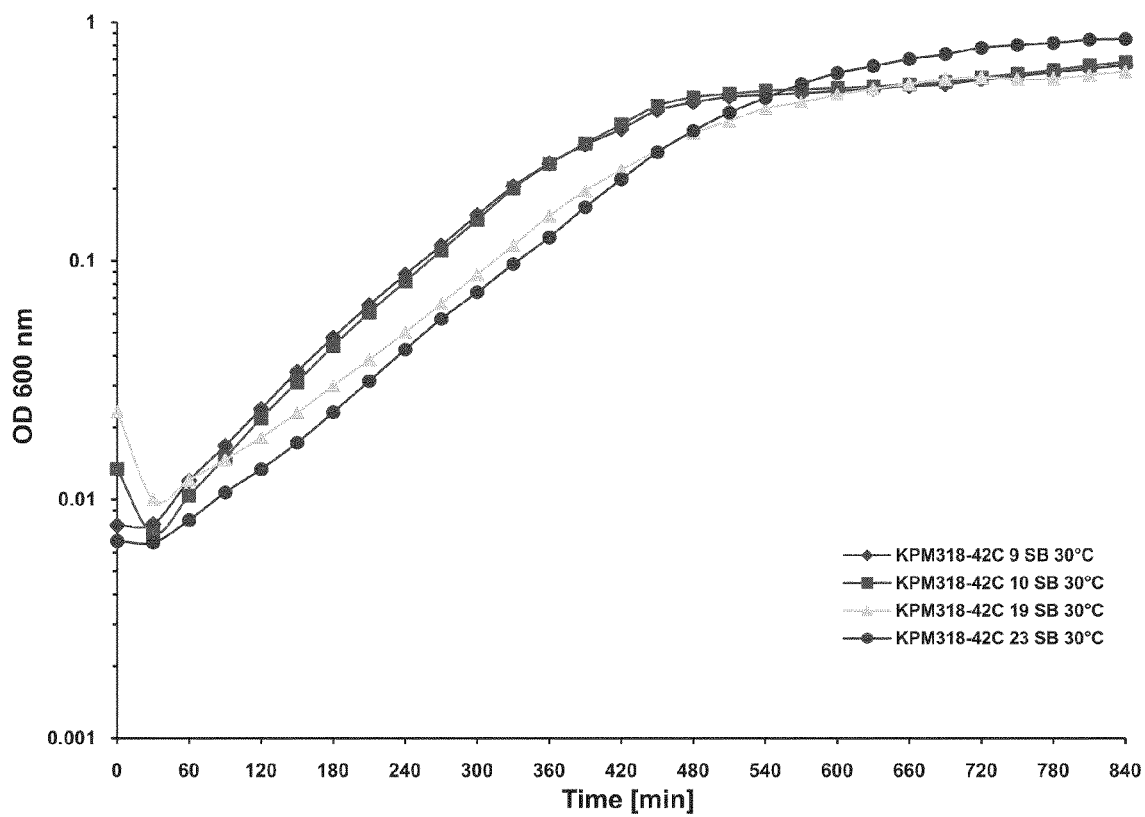


FIG. 16

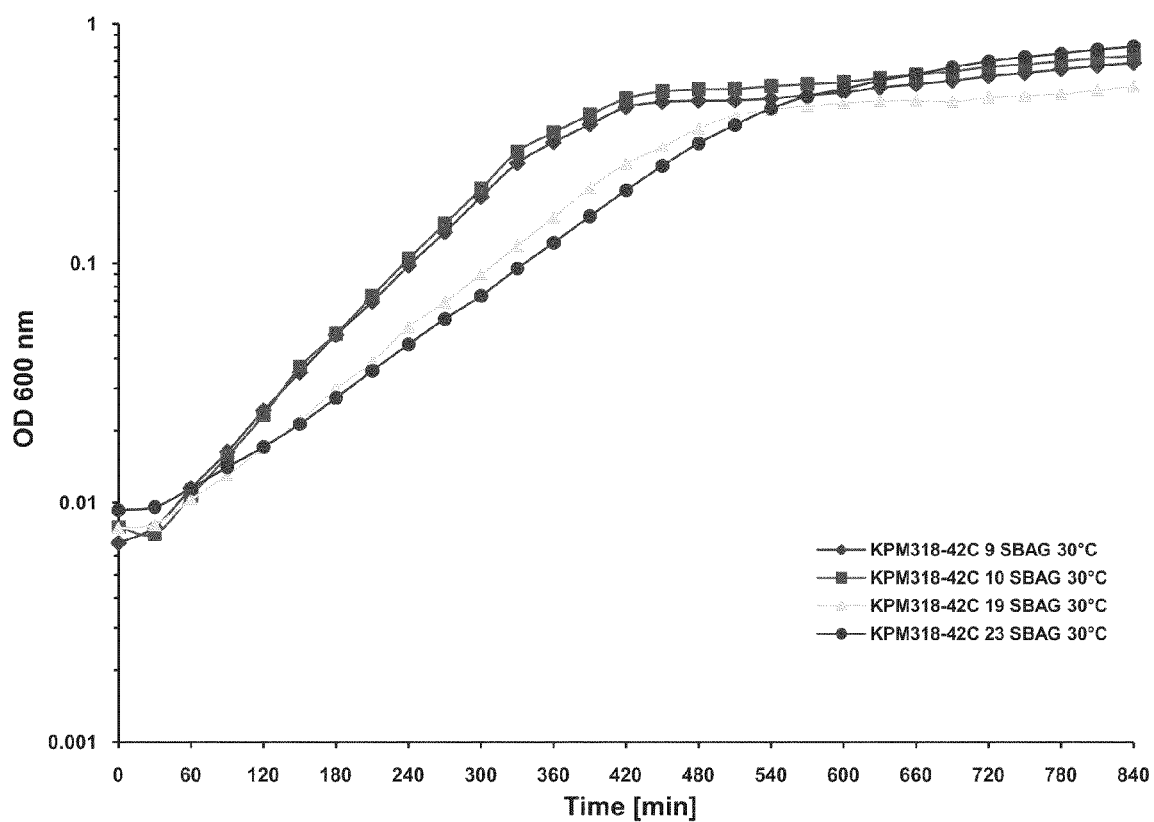


FIG. 17

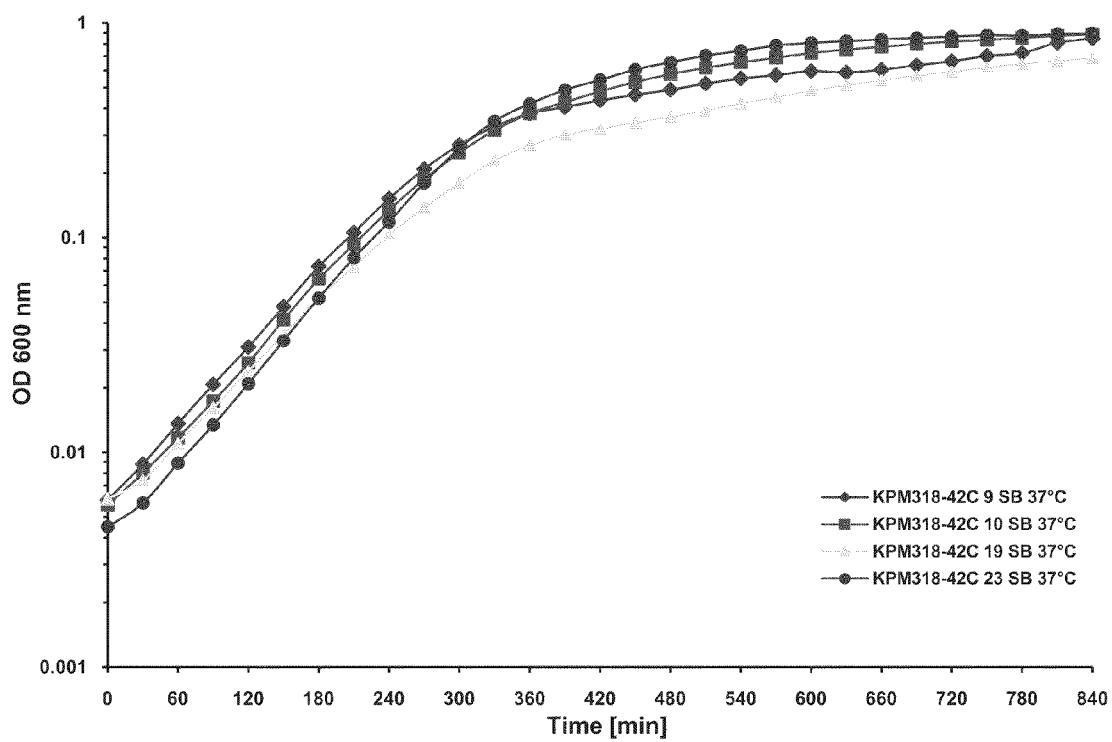


FIG. 18

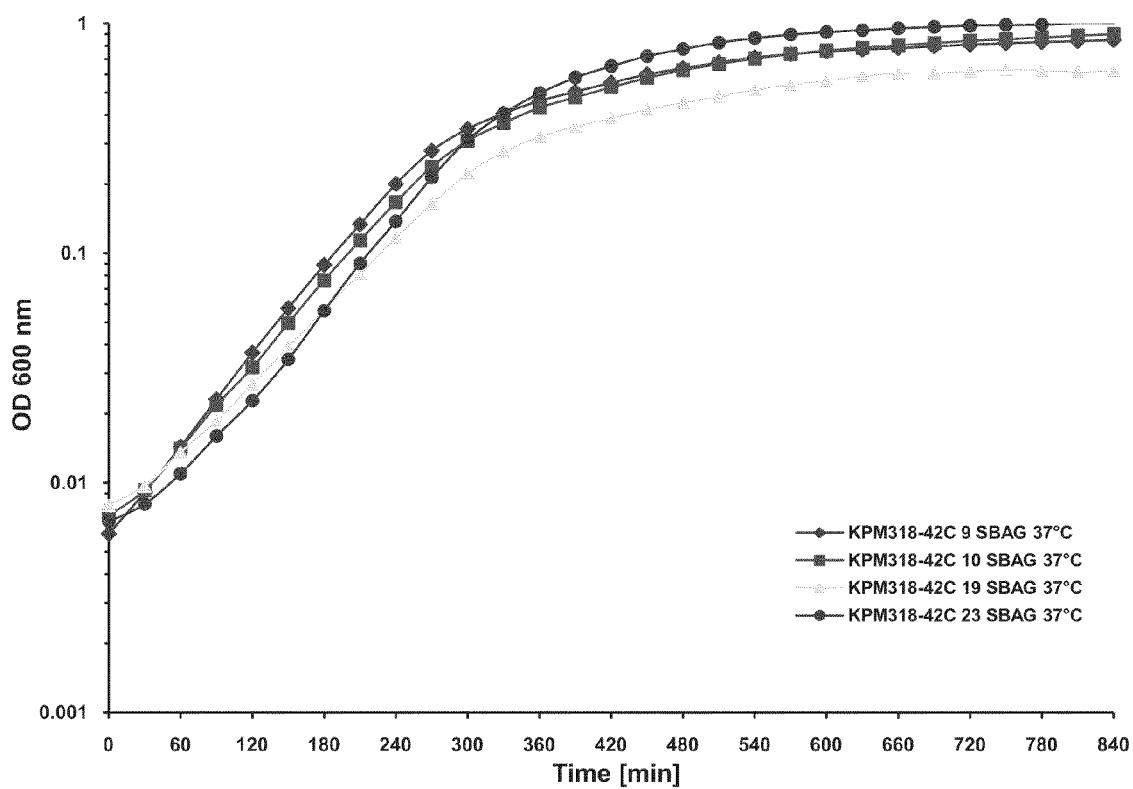


FIG. 19

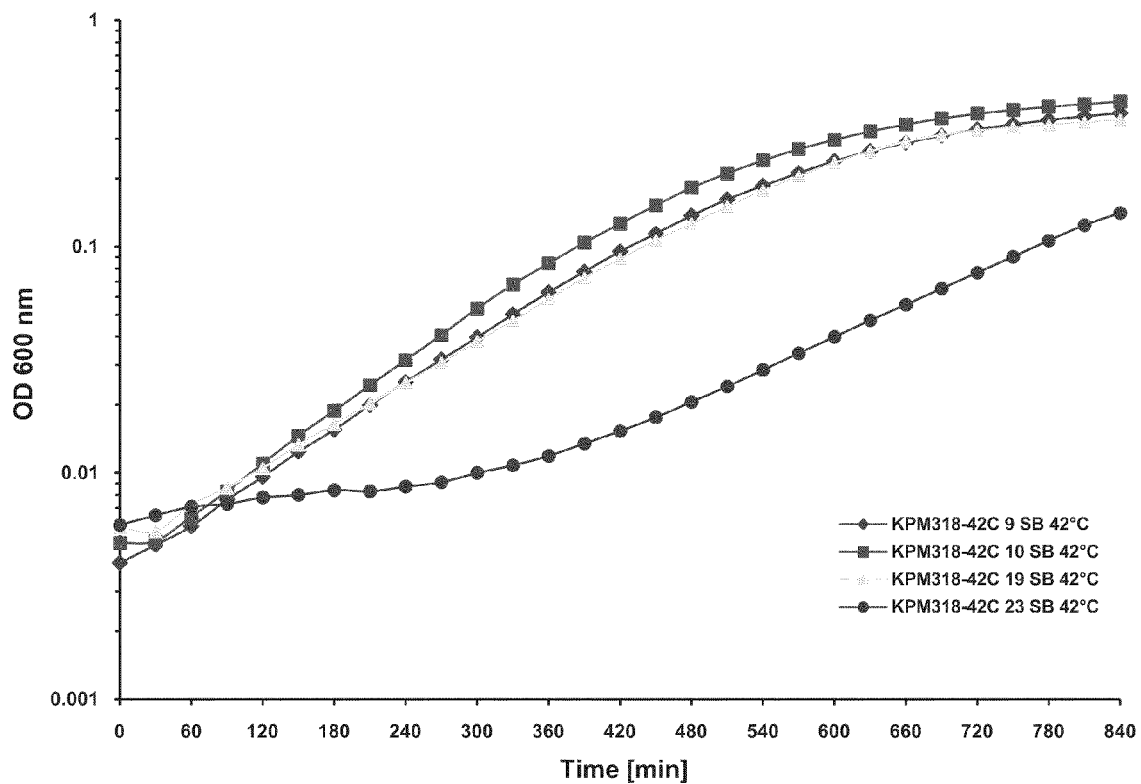


FIG. 20

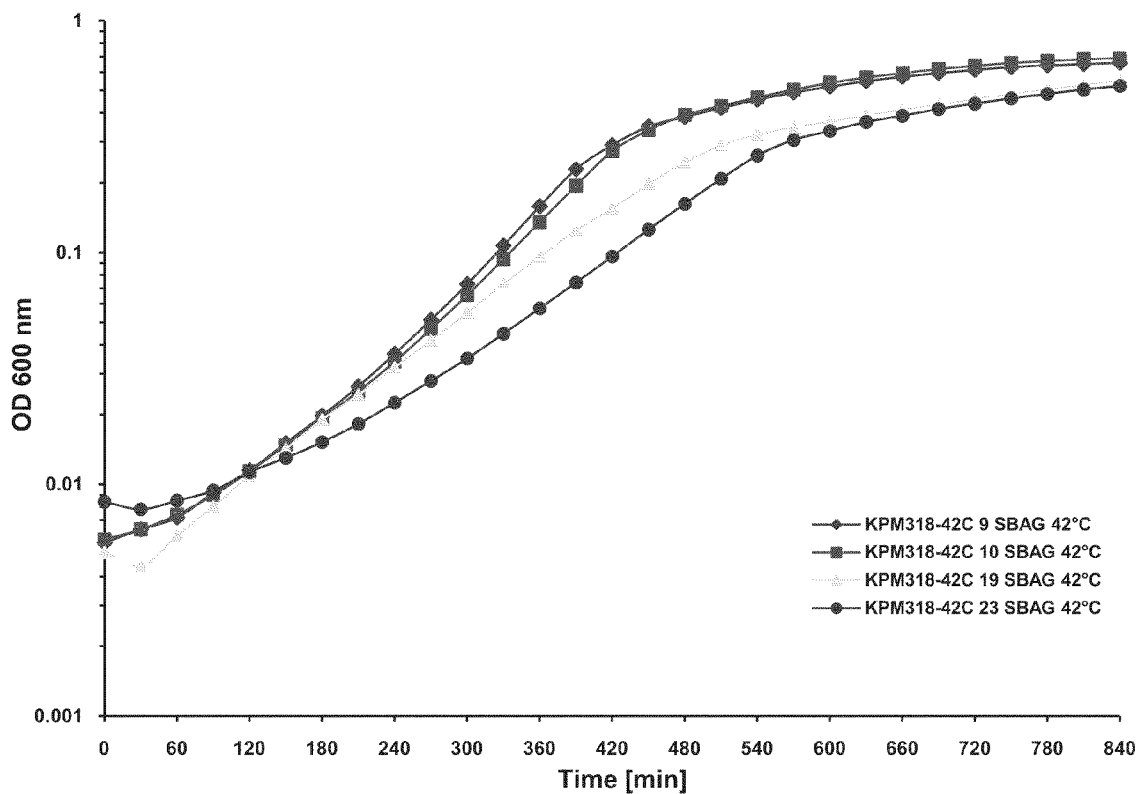


FIG. 21

KPM318-9										
SNP Calls										
Ref Position	Consens. position	Ref. Allele Base	Mut. Allele Base	Freq	#	tot #	Gene	Amino acid change	Effect	
193052	191000	G	T	100	30	30	<i>frr</i>	D61Y	altered ribosome recycling factor	UNIQUE to 9 & 10
547694	532079	A	G	100	16	16	<i>yibB</i>	E to E	<i>silent</i>	BW30270
965895	941032	C	T	100	19	19	<i>msbA</i>	P18S	known suppressor	KPM96
3188791	3128548	C	T	100	12	12	<i>yqii</i>	S to S	<i>silent</i>	KPMs
3644838	3571599	G	T	100	17	17	<i>gor</i>	V173F	altered glutathione oxidoreductase activity??	KPMs
3753464	3678094	G	C	100	17	17	<i>aldB</i>	T to T	<i>silent</i>	BW30270
3798895	3720172	T	A	100	10	10	<i>rfaY</i>	T32Y	altered LPS core sugar synthesis??	KPMs
3957957	3874474	C	T	100	10	10	none	?	no feature annotated	BW30270
DIP Calls										
del/insertion cost=2/2										
Ref Position	Consens. position	Ref. Allele Base	Mut. Allele Base	Freq	#	tot #	Gene	Change	Effect	
3558478	3490169	G	-	100	20	20	<i>glpR</i>	1 bp DEL	frameshift	BW30270

FIG. 22a

KPM318-10										
SNP Calls										
Ref Position	Consens. position	Ref. Allele Base	Mut. Allele Base	Freq	#	tot #	Gene	Amino acid change	Effect	
193052	191008	G	T	100	28	28	<i>frr</i>	D61Y	altered ribosome recycling factor	UNIQUE to 9 & 10
547694	532080	A	G	100	18	18	<i>yibB</i>	E to E	<i>silent</i>	BW30270
965895	941034	C	T	100	27	27	<i>msbA</i>	P18S	known suppressor	KPM96
3188791	3128576	C	T	100	13	13	<i>yqii</i>	S to S	<i>silent</i>	KPMs
3644838	3571685	G	T	100	19	19	<i>gor</i>	V173F	altered glutathione oxidoreductase activity??	KPMs
3753464	3678183	G	C	100	19	19	<i>aldB</i>	T to T	<i>silent</i>	BW30270
3798895	3720277	T	A	100	10	10	<i>rfaY</i>	T32Y	altered LPS core sugar synthesis??	KPMs
3957957	3874571	C	T	100	6	6	none	?	no feature annotated	BW30270
DIP Calls										
del/insertion cost=2/2										
Ref Position	Consens. position	Ref. Allele Base	Mut. Allele Base	Freq	#	tot #	Gene	Change	Effect	
3558478	3490381	G	-	100	20	20	<i>glpR</i>	1 bp DEL	frameshift	BW30270

FIG. 22b

KPM318-19

SNP Calls

Ref Position	Consens. position	Ref. Allele Base	Mut. Allele Base	Freq	#	tot #	Gene	Amino acid change	Effect	Lineage
547694	532090	A	G	100	20	20	yibB	E to E	silent	BW30270
965895	941050	C	T	100	17	17	msbA	P18S	known suppressor	KPM96
3188791	3128613	C	T	100	18	18	yqil	S to S	silent	KPMs
3644838	3571682	G	T	100	16	16	gor	V173F	altered glutathione oxidoreductase?	KPMs
3753464	3678174	G	C	100	19	19	aldB	T to T	silent	BW30270
3798895	3720279	T	A	100	10	10	rfaY	T32Y	altered LPS core sugar synthesis??	KPMs
3957957	3874575	C	T	100	12	12	none	?	no feature annotated	BW30270

DIP Calls

Ref pos	Consens pos	Ref Base	Var Base(s)	Freq	#	tot #	Gene	Change	Effect	Lineage
3558478	3490283	G		100	21	21	glpR	1 bp DEL	frameshift	BW30270
4373919	4271896	-	T	100	38	38	efp		frameshift in elongation factor P	THIS ISOLATE - BEST CANDIDATE FOR PHENOTYPE

FIG. 22c

KPM318-23

SNP Calls

Ref Position	Consens. position	Ref. Allele Base	Mut. Allele Base	Freq	#	tot #	Gene	Amino acid change	Effect	Lineage
547694	532099	A	G	100	27	27	<i>yibB</i>	E to E	silent	BW30270
965895	941061	C	T	100	25	25	<i>msbA</i>	P18S	known suppressor	KPM96
3188791	3128668	C	T	100	8	8	<i>yqiI</i>	S to S	silent	KPMs
3644838	3571751	G	T	100	23	23	<i>gor</i>	V173F	altered glutathione oxidoreductas e activity??	KPMs
3753464	3678248	G	C	100	35	35	<i>aldB</i>	T to T	silent	BW30270
3798895	3720343	T	A	100	12	12	<i>rfaY</i>	T32Y	altered LPS core sugar synthesis??	KPMs
3937957	3874633	C	T	100	8	8	none	?	no feature annotated	BW30270

DIP Calls

Ref pos	Consens pos	Ref Base	Var Base(s)	Freq	#	tot #	Gene	Change	Effect	Lineage
2139799	2095371	CAGCGG	-	100	10	10	<i>dcd</i>	PLPLAL to PLAL	2 AA deletion	UNIQUE
3558478	3490307	G	-	100	35	35	<i>glpR</i>	1 bp DEL	frameshift	BW30270

FIG. 22d

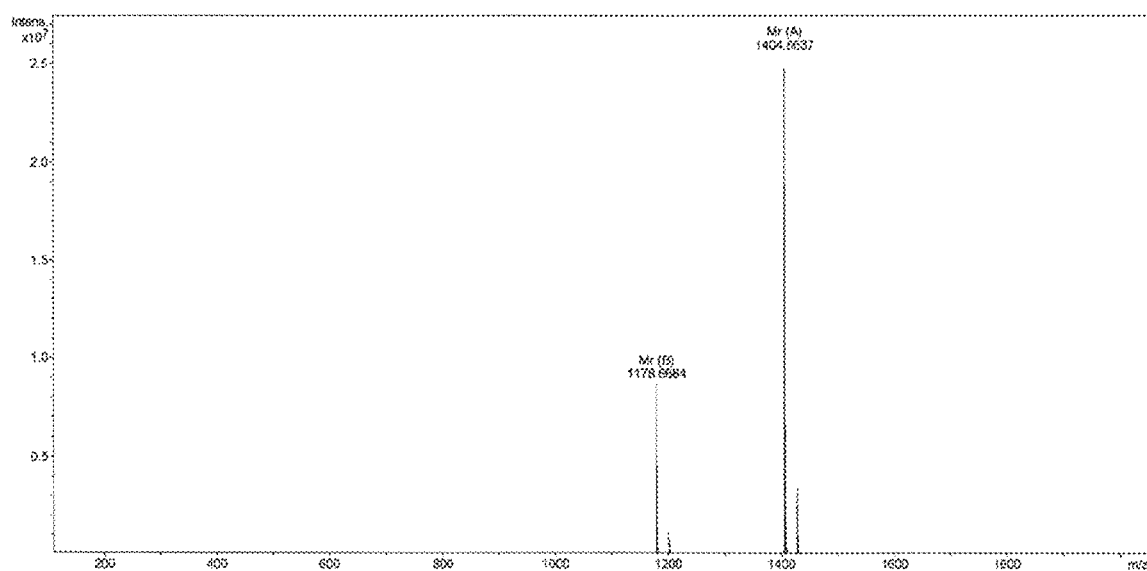


FIG. 23

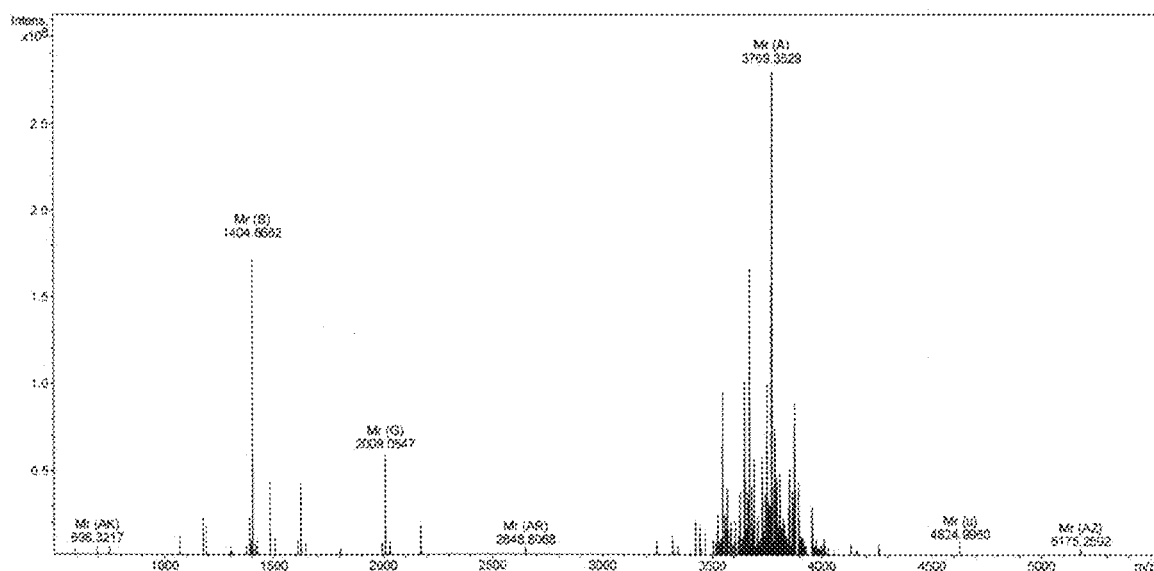


FIG. 24

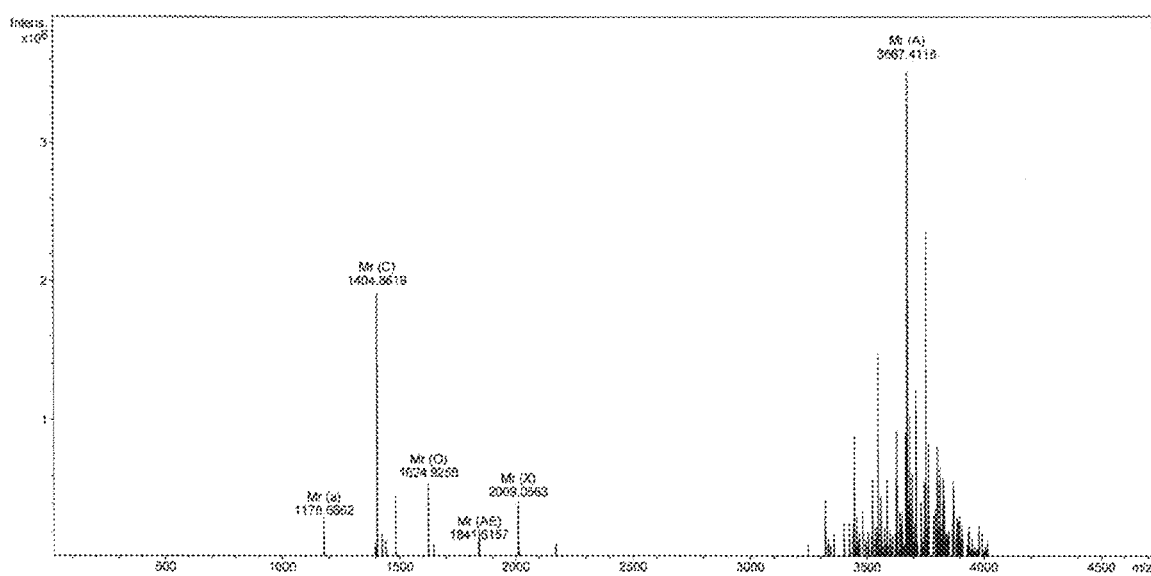


FIG. 25

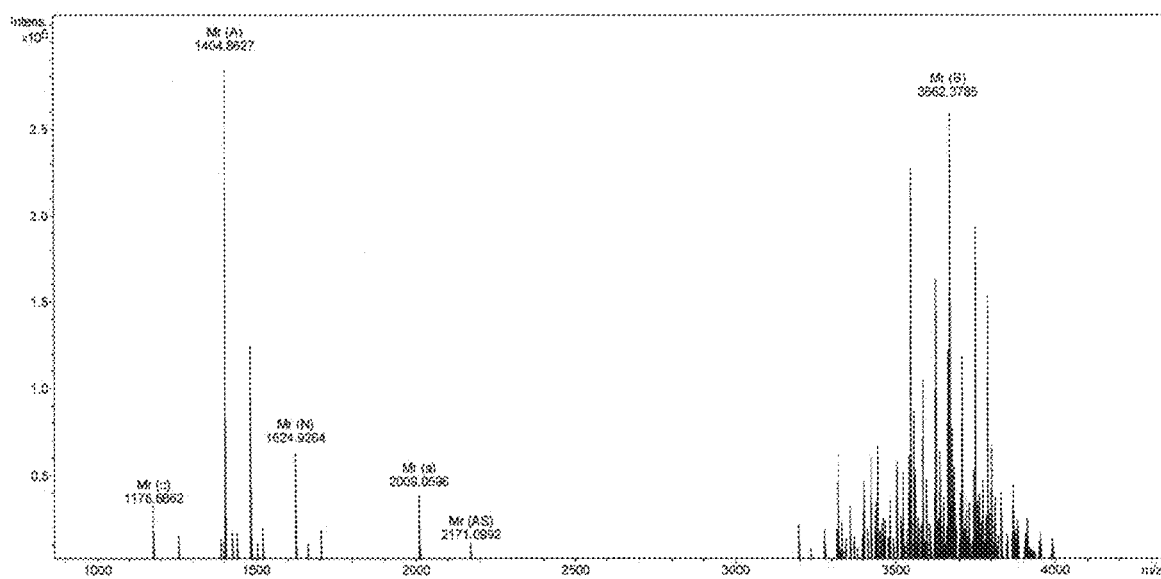


FIG. 26

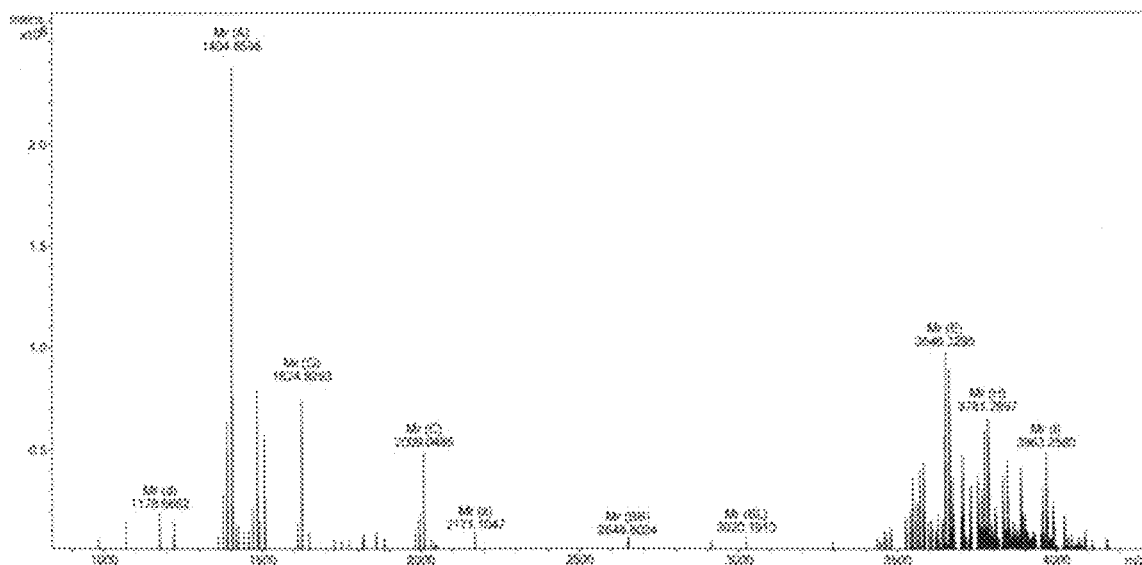


FIG. 27

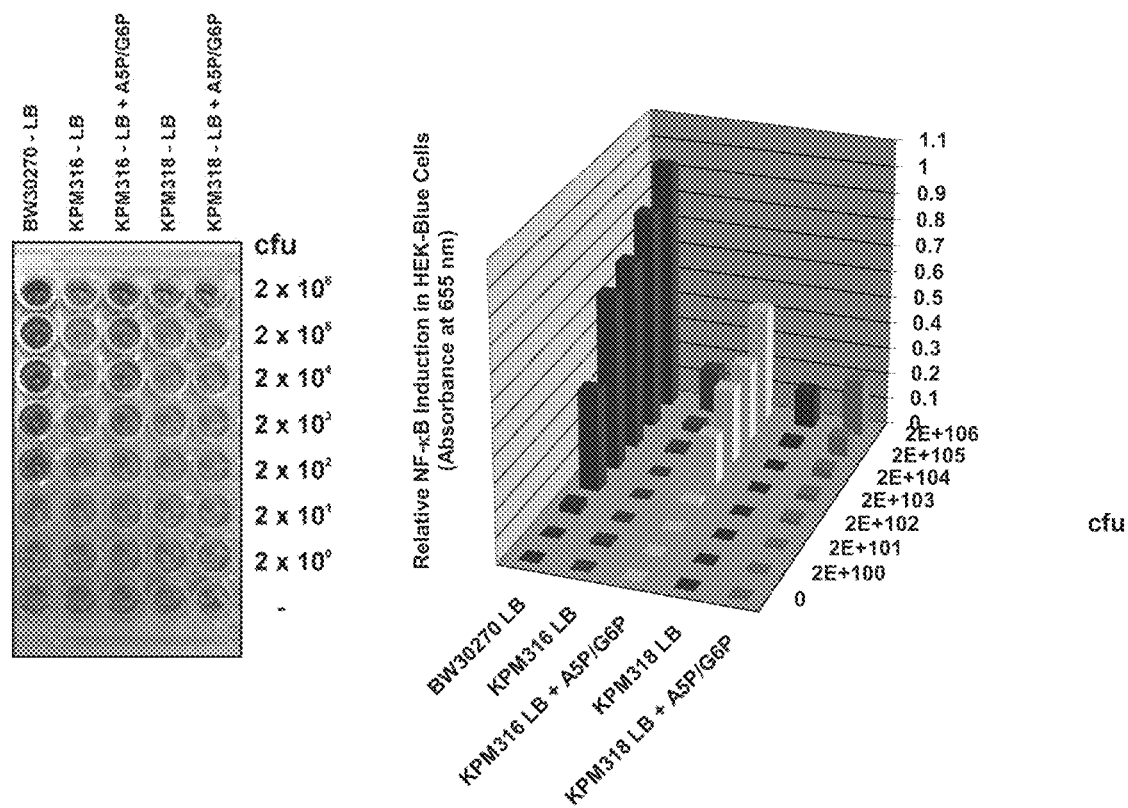


FIG. 28

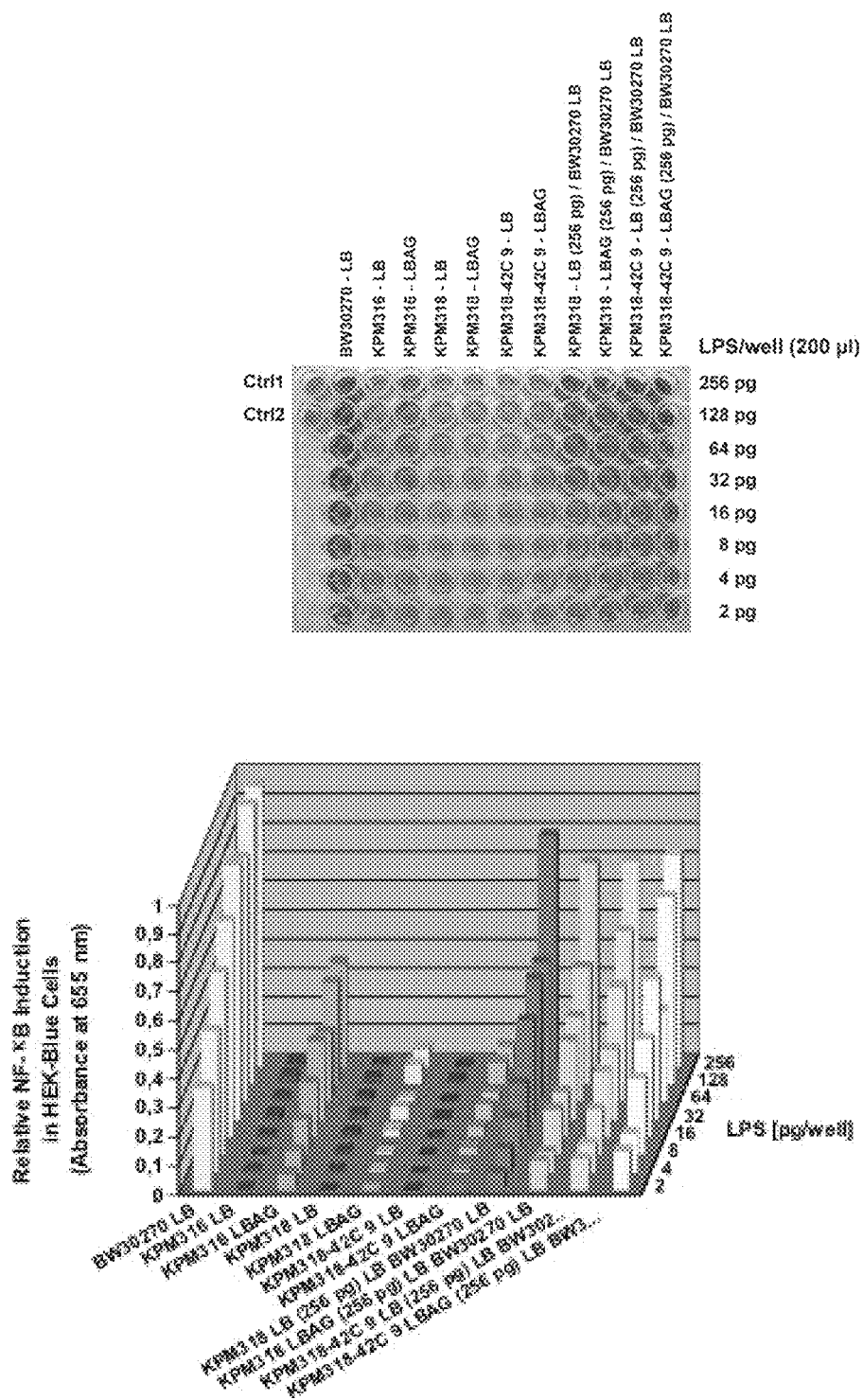


FIG. 29

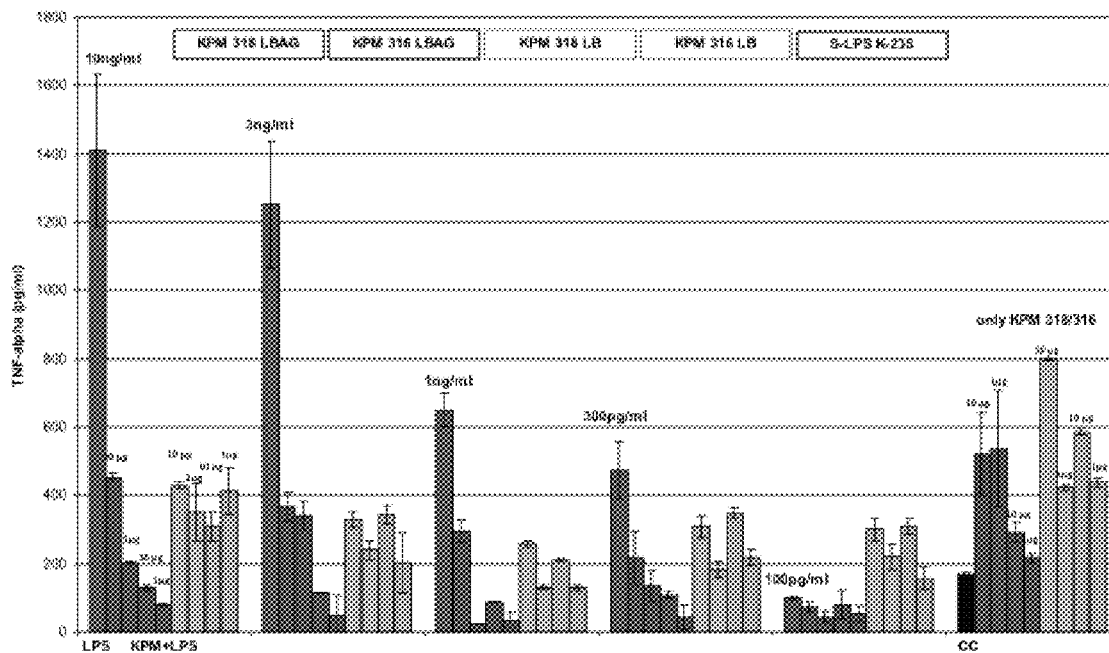


FIG. 30



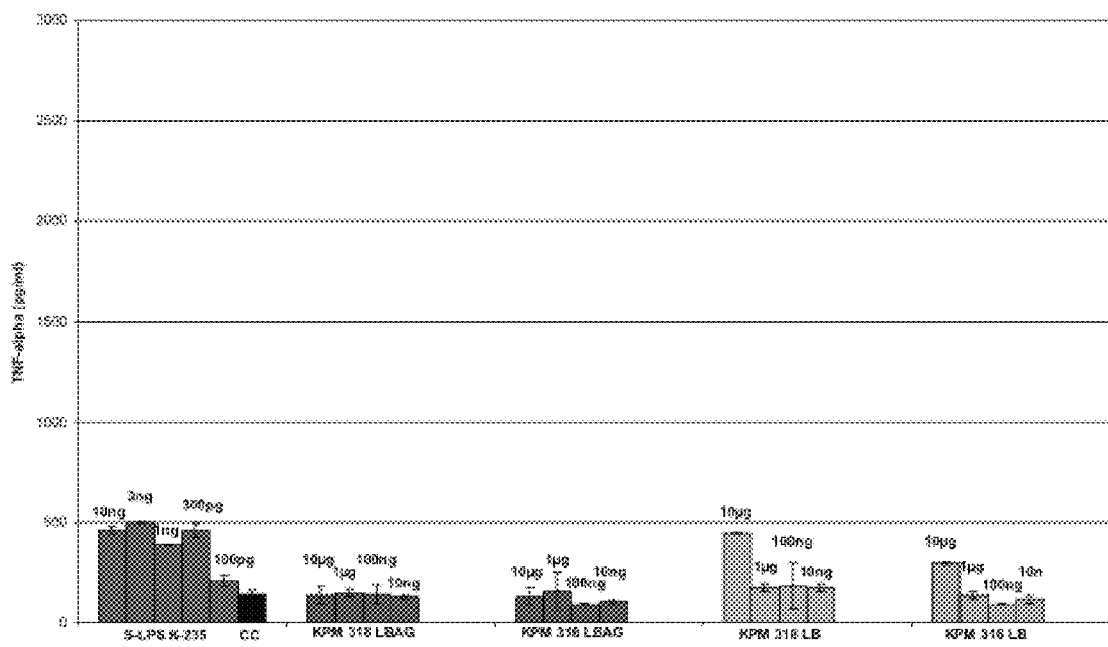


FIG. 32

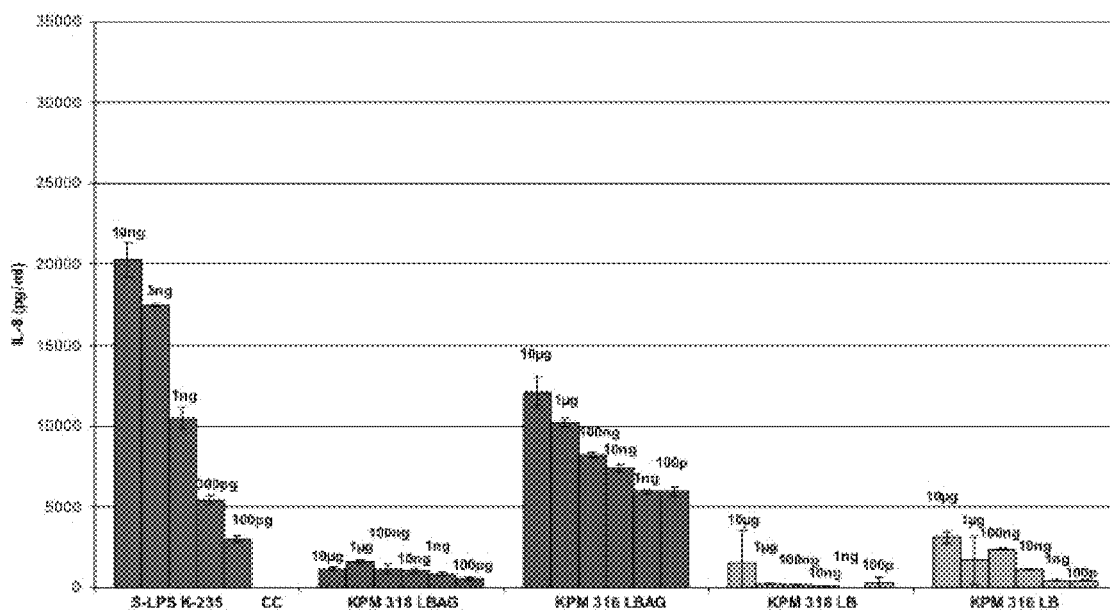


FIG. 33

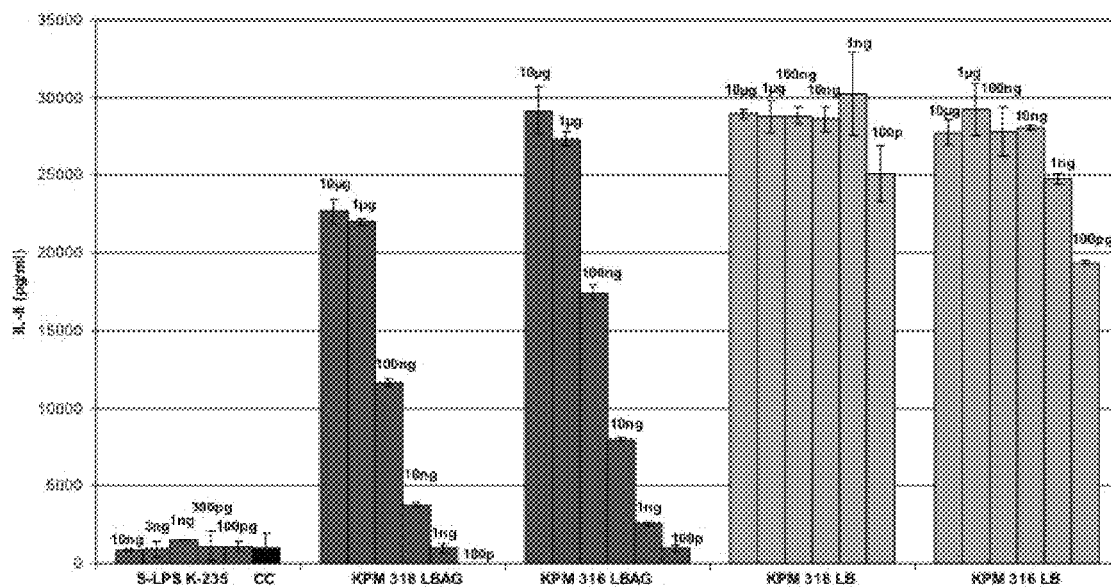


FIG. 34

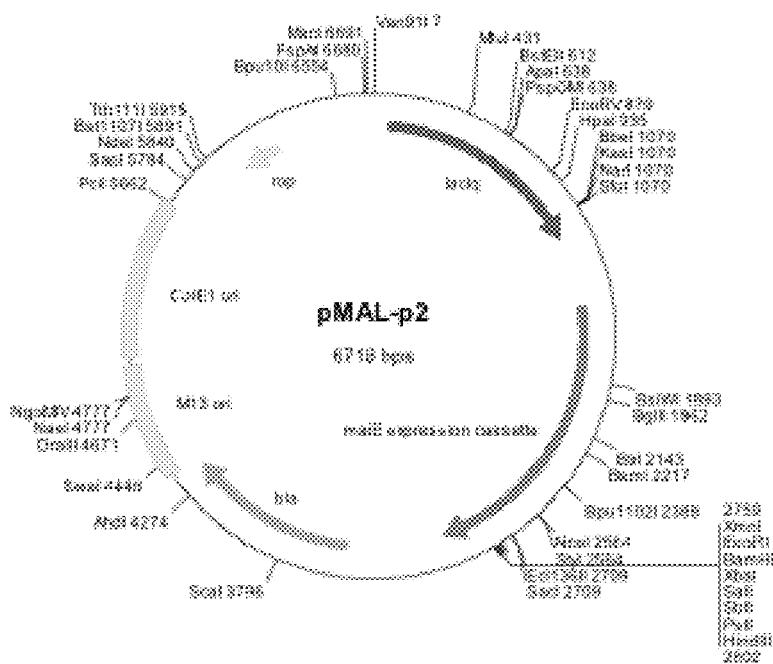
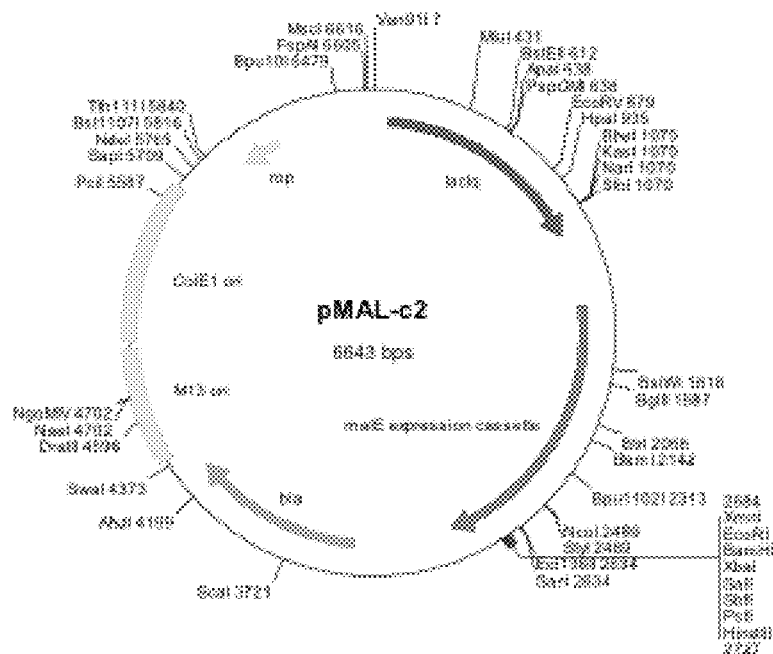
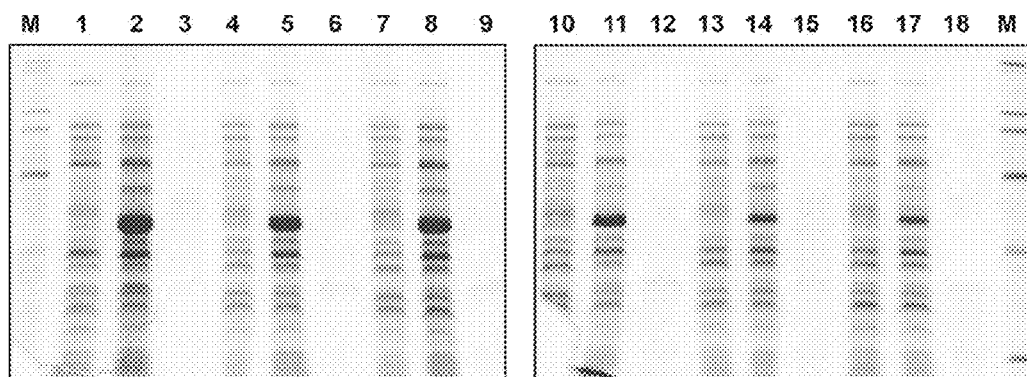
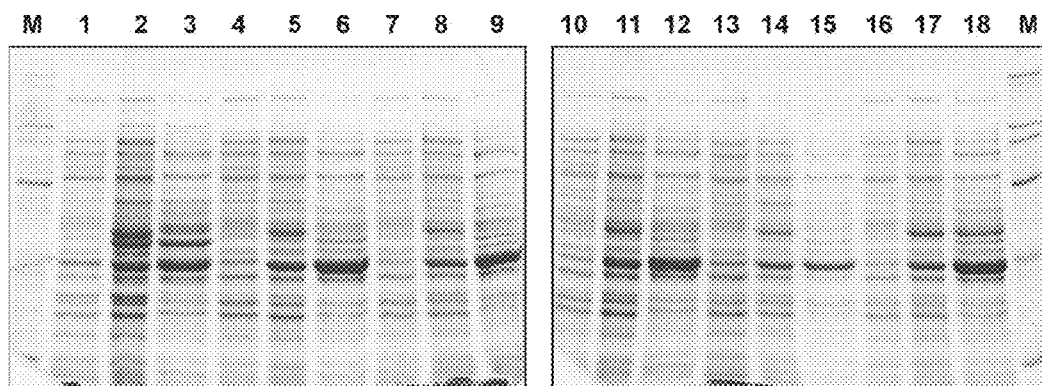


FIG. 35



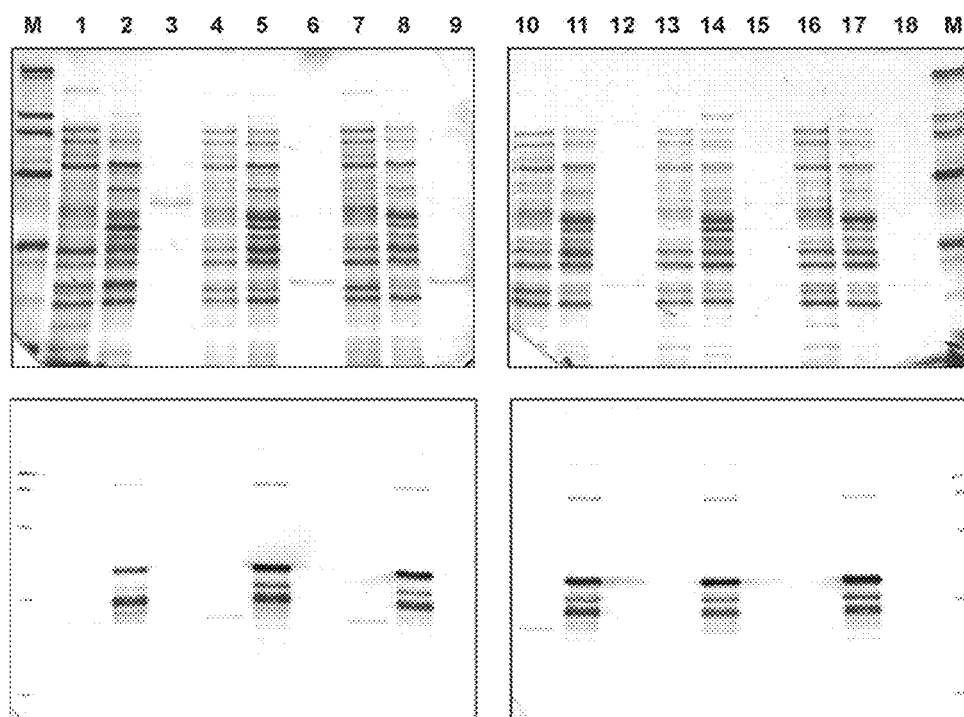
1. BW30270/pMAL-c2 - uninduced
2. BW30270/pMAL-c2 – protein extract, induced (3h)
3. BW30270/pMAL-c2 – culture supernatant, induced (overnight)
4. KPM318/pMAL-c2 - uninduced
5. KPM318/pMAL-c2 – protein extract, induced (3h)
6. KPM318/pMAL-c2 – culture supernatant, induced (overnight)
7. KPM318-9/pMAL-c2 – uninduced
8. KPM318-9/pMAL-c2 – protein extract, induced (3h)
9. KPM318-9/pMAL-c2 – culture supernatant, induced (overnight)
10. KPM318-10/pMAL-c2 – uninduced
11. KPM318-10/pMAL-c2 – protein extract, induced (3h)
12. KPM318-10/pMAL-c2 – culture supernatant, induced (overnight)
13. KPM318-19/pMAL-c2 – uninduced
14. KPM318-19/pMAL-c2 – protein extract, induced (3h)
15. KPM318-19/pMAL-c2 – culture supernatant, induced (overnight)
16. KPM318-23/pMAL-c2 – uninduced
17. KPM318-23/pMAL-c2 – protein extract, induced (3h)
18. KPM318-23/pMAL-c2 – culture supernatant, induced (overnight)

FIG. 36



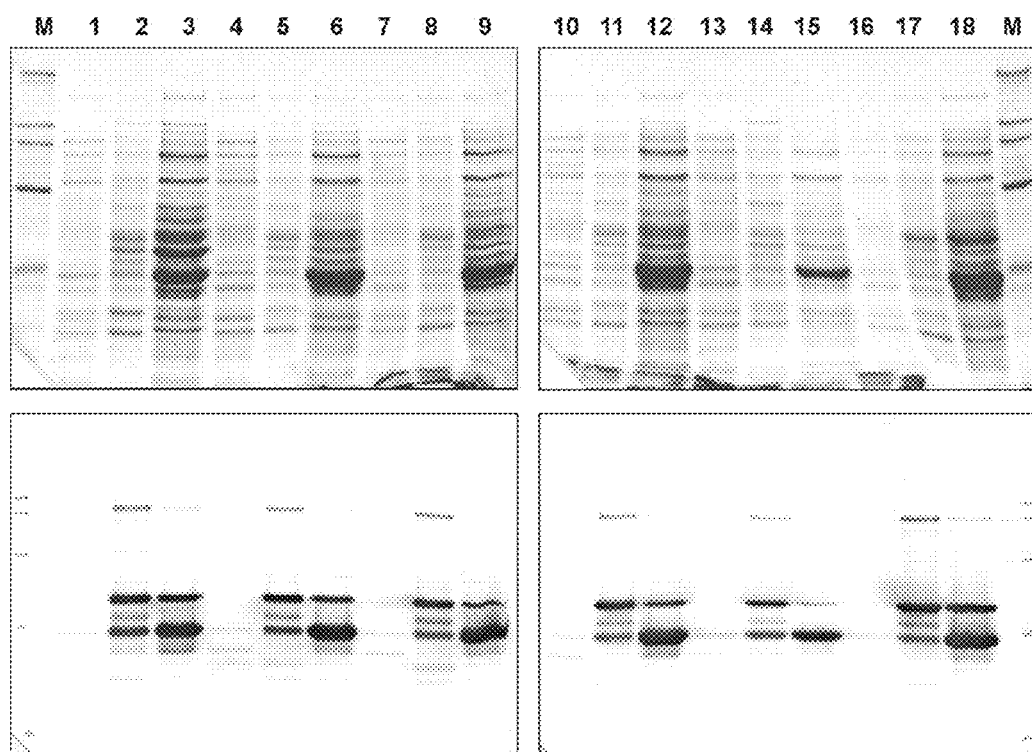
1. BW30270/pMAL-p2 - uninduced
2. BW30270/pMAL-p2 – protein extract, induced (3h)
3. BW30270/pMAL-p2 – culture supernatant, induced (overnight)
4. KPM318/pMAL-p2 - uninduced
5. KPM318/pMAL-p2 – protein extract, induced (3h)
6. KPM318/pMAL-p2 – culture supernatant, induced (overnight)
7. KPM318-9/pMAL-p2 – uninduced
8. KPM318-9/pMAL-p2 – protein extract, induced (3h)
9. KPM318-9/pMAL-p2 – culture supernatant, induced (overnight)
10. KPM318-10/pMAL-p2 – uninduced
11. KPM318-10/pMAL-p2 – protein extract, induced (3h)
12. KPM318-10/pMAL-p2 – culture supernatant, induced (overnight)
13. KPM318-19/pMAL-p2 – uninduced
14. KPM318-19/pMAL-p2 – protein extract, induced (3h)
15. KPM318-19/pMAL-p2 – culture supernatant, induced (overnight)
16. KPM318-23/pMAL-p2 – uninduced
17. KPM318-23/pMAL-p2 – protein extract, induced (3h)
18. KPM318-23/pMAL-p2 – culture supernatant, induced (overnight)

FIG. 37



1. BW30270/pMAL-c2 - uninduced
2. BW30270/pMAL-c2 – protein extract, induced (overnight)
3. BW30270/pMAL-c2 – culture supernatant, induced (overnight)
4. KPM318/pMAL-c2 - uninduced
5. KPM318/pMAL-c2 – protein extract, induced (overnight)
6. KPM318/pMAL-c2 – culture supernatant, induced (overnight)
7. KPM318-9/pMAL-c2 – uninduced
8. KPM318-9/pMAL-c2 – protein extract, induced (overnight)
9. KPM318-9/pMAL-c2 – culture supernatant, induced (overnight)
10. KPM318-10/pMAL-c2 – uninduced
11. KPM318-10/pMAL-c2 – protein extract, induced (overnight)
12. KPM318-10/pMAL-c2 – culture supernatant, induced (overnight)
13. KPM318-19/pMAL-c2 – uninduced
14. KPM318-19/pMAL-c2 – protein extract, induced (overnight)
15. KPM318-19/pMAL-c2 – culture supernatant, induced (overnight)
16. KPM318-23/pMAL-c2 – uninduced
17. KPM318-23/pMAL-c2 – protein extract, induced (overnight)
18. KPM318-23/pMAL-c2 – culture supernatant, induced (overnight)

FIG. 38



1. BW30270/pMAL-p2 - uninduced
2. BW30270/pMAL-p2 – protein extract, induced (overnight)
3. BW30270/pMAL-p2 – culture supernatant, induced (overnight)
4. KPM318/pMAL-p2 - uninduced
5. KPM318/pMAL-p2 – protein extract, induced (overnight)
6. KPM318/pMAL-p2 – culture supernatant, induced (overnight)
7. KPM318-9/pMAL-p2 – uninduced
8. KPM318-9/pMAL-p2 – protein extract, induced (overnight)
9. KPM318-9/pMAL-p2 – culture supernatant, induced (overnight)
10. KPM318-10/pMAL-p2 – uninduced
11. KPM318-10/pMAL-p2 – protein extract, induced (overnight)
12. KPM318-10/pMAL-p2 – culture supernatant, induced (overnight)
13. KPM318-19/pMAL-p2 – uninduced
14. KPM318-19/pMAL-p2 – protein extract, induced (overnight)
15. KPM318-19/pMAL-p2 – culture supernatant, induced (overnight)
16. KPM318-23/pMAL-p2 – uninduced
17. KPM318-23/pMAL-p2 – protein extract, induced (overnight)
18. KPM318-23/pMAL-p2 – culture supernatant, induced (overnight)

FIG. 39

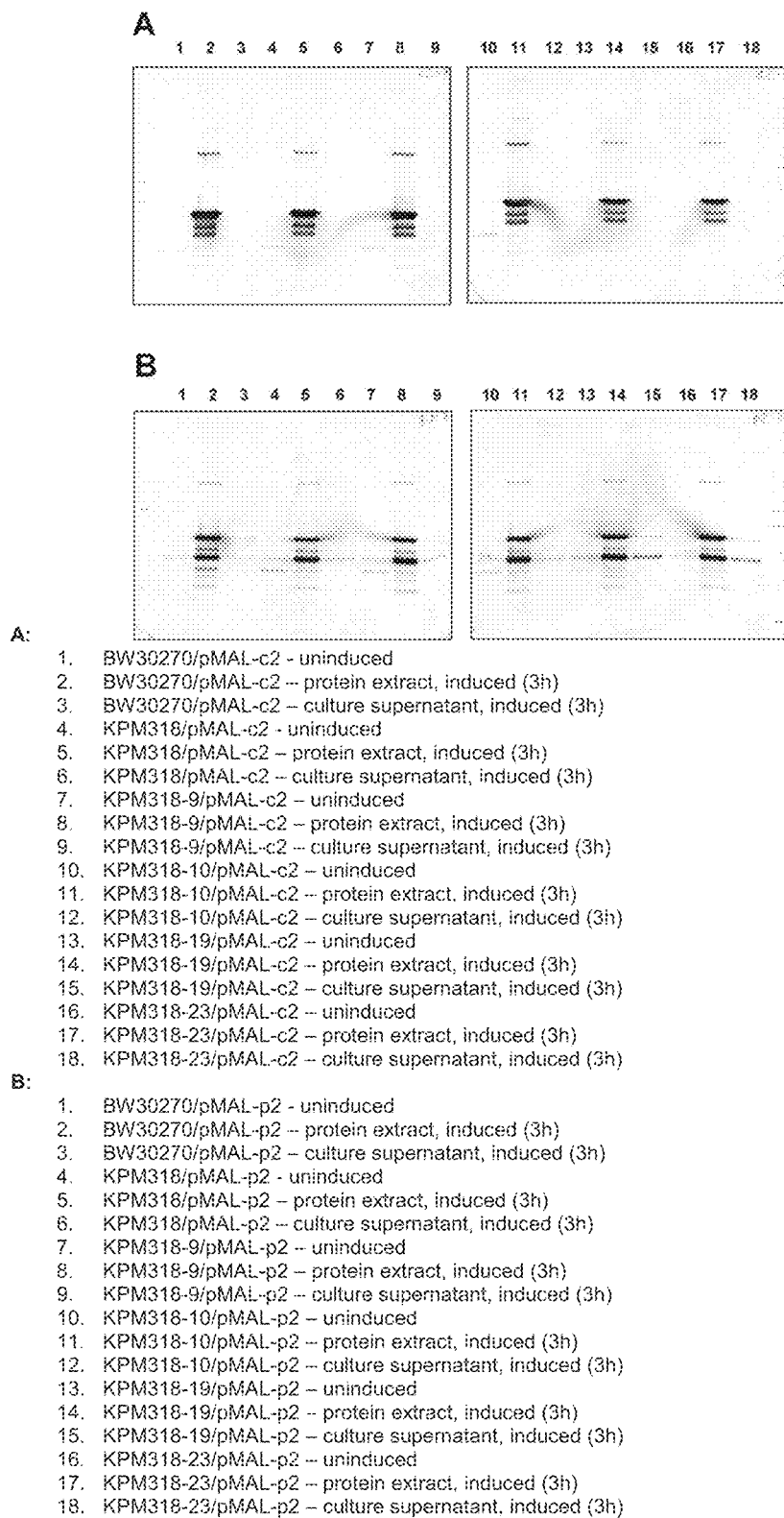
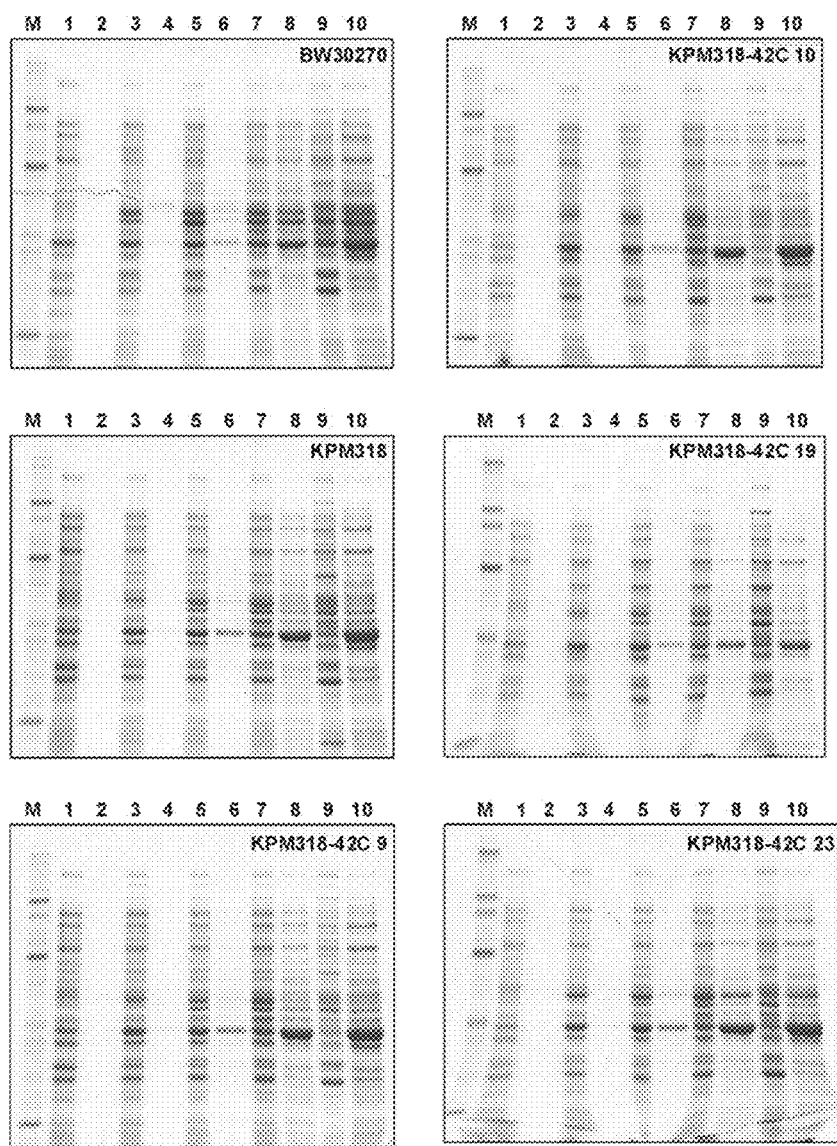
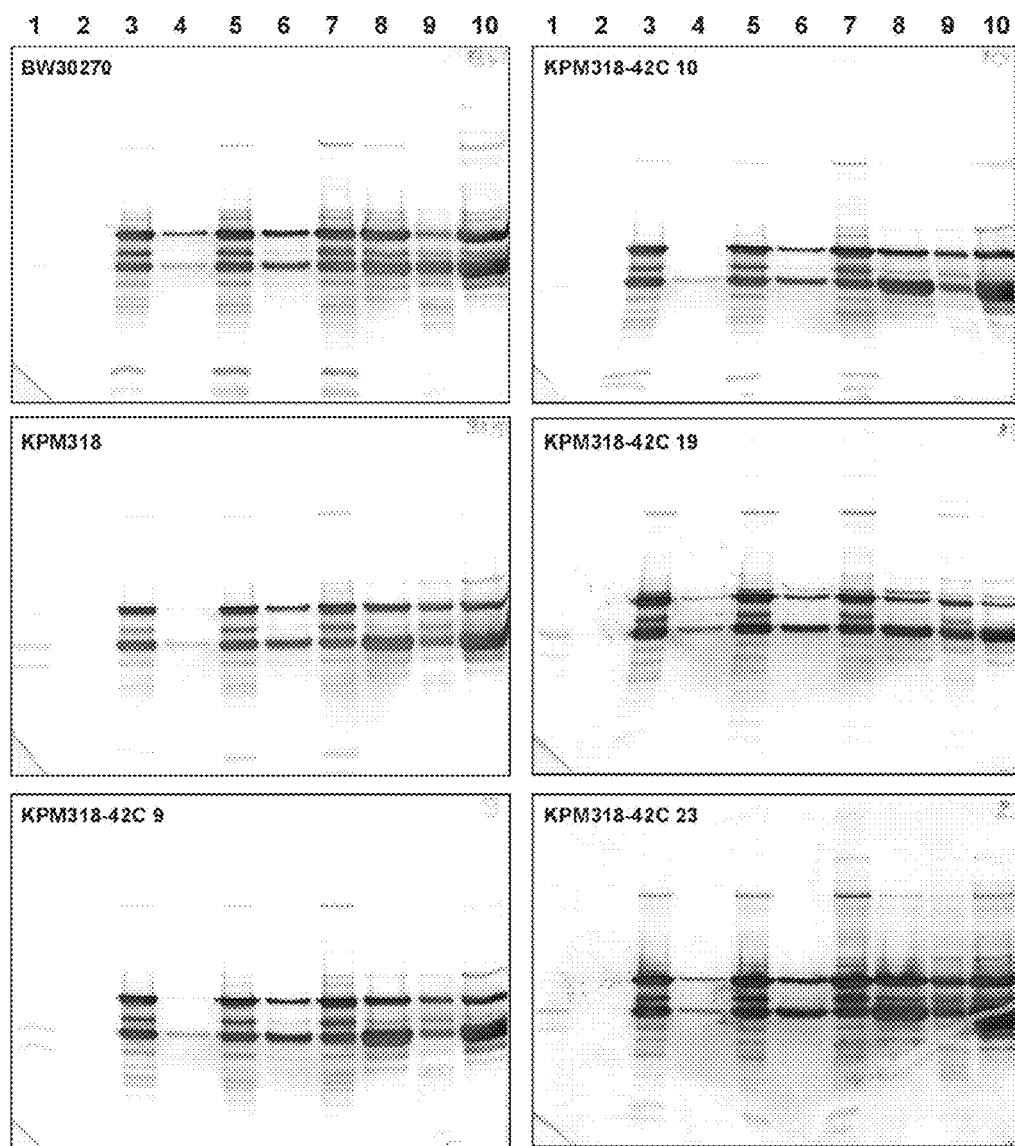


FIG. 40



1. Protein extract - uninduced
2. Culture supernatant - uninduced
3. Protein extract - induced (3h)
4. Culture supernatant - induced (3h)
5. Protein extract - induced (6h)
6. Culture supernatant - induced (6h)
7. Protein extract - induced (12h)
8. Culture supernatant - induced (12h)
9. Protein extract - induced (24h)
10. Culture supernatant - induced (24h)

FIG. 41



1. Protein extract – uninduced
2. Culture supernatant – uninduced
3. Protein extract – induced (3h)
4. Culture supernatant – induced (3h)
5. Protein extract – induced (6h)
6. Culture supernatant – induced (6h)
7. Protein extract – induced (12h)
8. Culture supernatant – induced (12h)
9. Protein extract – induced (24h)
10. Culture supernatant – induced (24h)

FIG. 42

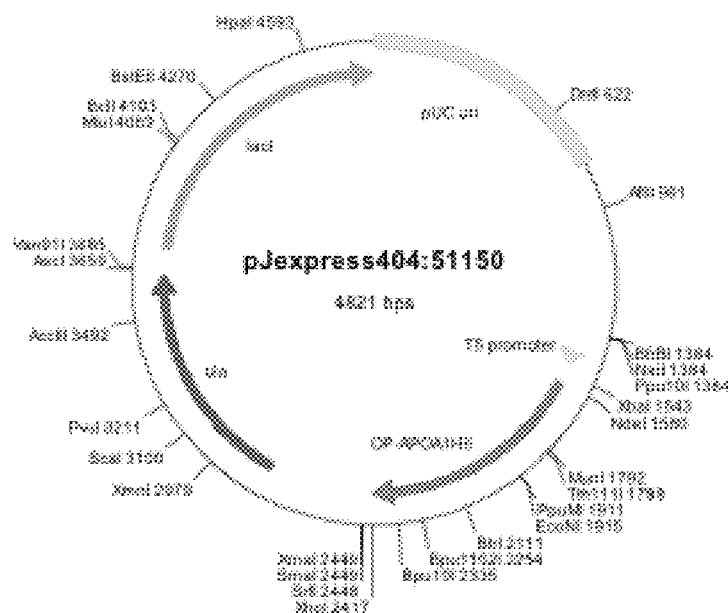
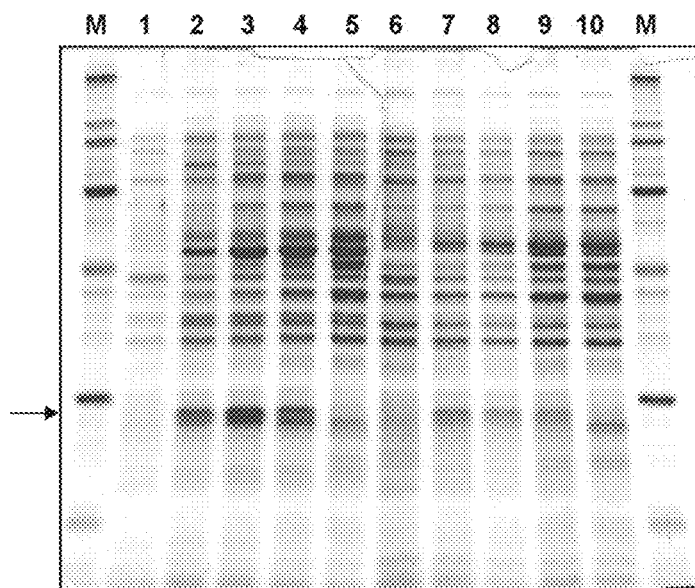
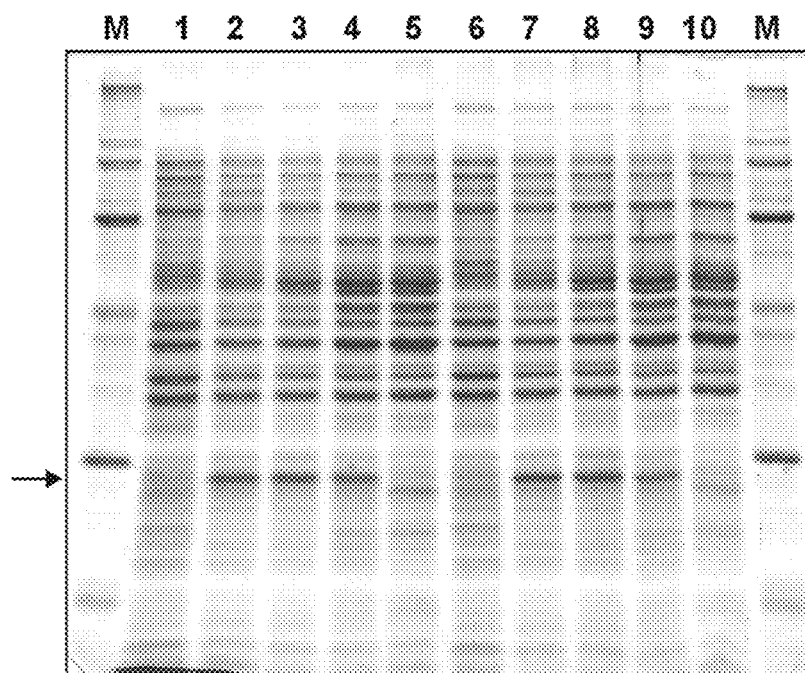


FIG. 43



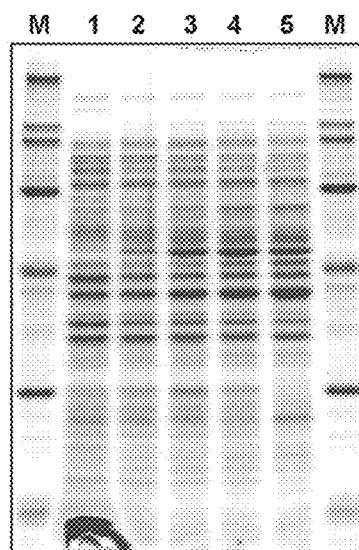
1. BW30270/pJexpress404:51149 - uninduced
2. BW30270/pJexpress404:51149 - induced (3 h)
3. BW30270/pJexpress404:51149 - induced (6 h)
4. BW30270/pJexpress404:51149 - induced (12 h)
5. BW30270/pJexpress404:51149 - induced (24 h)
6. KPM318/pJexpress404:51149 - uninduced
7. KPM318/pJexpress404:51149 - induced (3 h)
8. KPM318/pJexpress404:51149 - induced (6 h)
9. KPM318/pJexpress404:51149 - induced (12 h)
10. KPM318/pJexpress404:51149 - induced (24 h)

FIG. 44



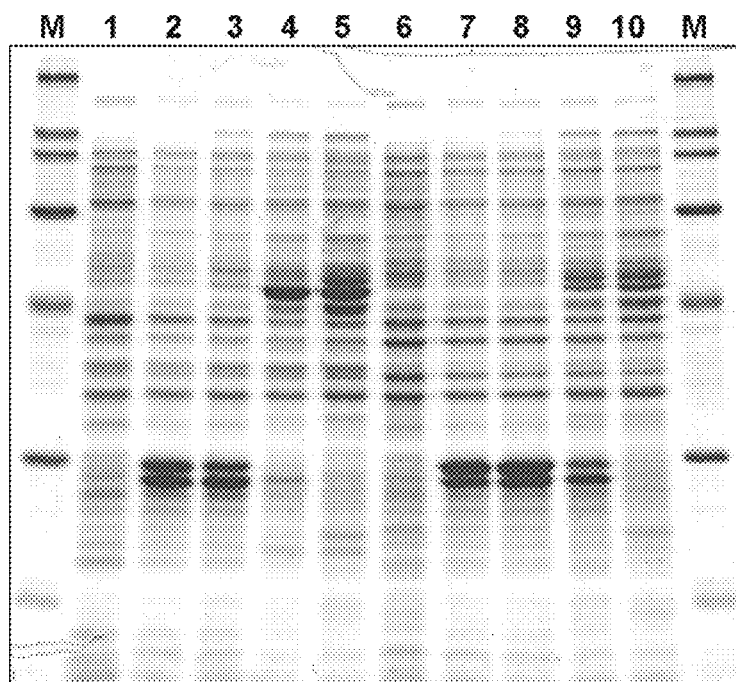
1. KPM318-9/pJexpress404:51149 - uninduced
2. KPM318-9/pJexpress404:51149 - induced (3 h)
3. KPM318-9/pJexpress404:51149 - induced (6 h)
4. KPM318-9/pJexpress404:51149 - induced (12 h)
5. KPM318-9/pJexpress404:51149 - induced (24 h)
6. KPM318-10/pJexpress404:51149 - uninduced
7. KPM318-10/pJexpress404:51149 - induced (3 h)
8. KPM318-10/pJexpress404:51149 - induced (6 h)
9. KPM318-10/pJexpress404:51149 - induced (12 h)
10. KPM318-10/pJexpress404:51149 - induced (24 h)

FIG. 45



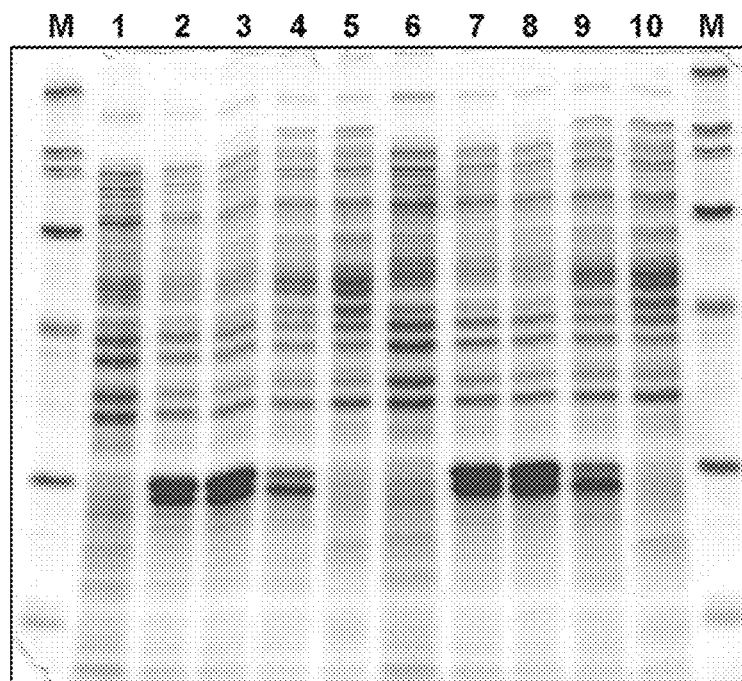
1. KPM318-19/pJexpress404:51149 – uninduced
2. KPM318-19/pJexpress404:51149 - induced (3 h)
3. KPM318-19/pJexpress404:51149 - induced (6 h)
4. KPM318-19/pJexpress404:51149 - induced (12 h)
5. KPM318-19/pJexpress404:51149 - induced (24 h)

FIG. 46



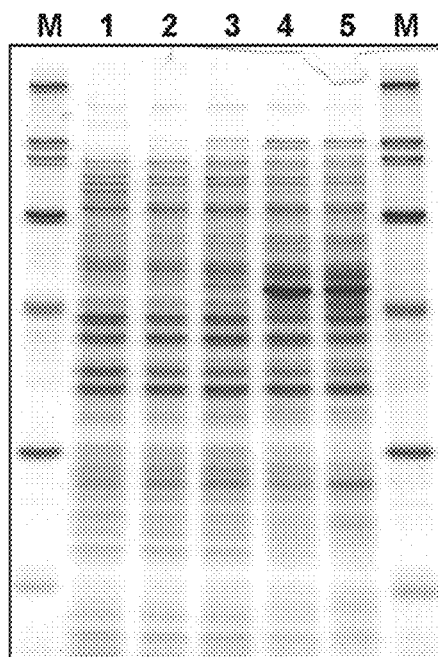
1. BW30270/pJexpress404:51150 - uninduced
2. BW30270/pJexpress404:51150 - induced (3 h)
3. BW30270/pJexpress404:51150 - induced (6 h)
4. BW30270/pJexpress404:51150 - induced (12 h)
5. BW30270/pJexpress404:51150 - induced (24 h)
6. KPM318/pJexpress404:51150 - uninduced
7. KPM318/pJexpress404:51150 - induced (3 h)
8. KPM318/pJexpress404:51150 - induced (6 h)
9. KPM318/pJexpress404:51150 - induced (12 h)
10. KPM318/pJexpress404:51150 - induced (24 h)

FIG. 47



1. KPM318-9/pJexpress404:51150 - uninduced
2. KPM318-9/pJexpress404:51150 - induced (3 h)
3. KPM318-9/pJexpress404:51150 - induced (6 h)
4. KPM318-9/pJexpress404:51150 - induced (12 h)
5. KPM318-9/pJexpress404:51150 - induced (24 h)
6. KPM318-10/pJexpress404:51150 - uninduced
7. KPM318-10/pJexpress404:51150 - induced (3 h)
8. KPM318-10/pJexpress404:51150 - induced (6 h)
9. KPM318-10/pJexpress404:51150 - induced (12 h)
10. KPM318-10/pJexpress404:51150 - induced (24 h)

FIG. 48



1. KPM318-19/pJexpress404:51150 – uninduced
2. KPM318-19/pJexpress404:51150 - induced (3 h)
3. KPM318-19/pJexpress404:51150 - induced (6 h)
4. KPM318-19/pJexpress404:51150 - induced (12 h)
5. KPM318-19/pJexpress404:51150 - induced (24 h)

FIG. 49

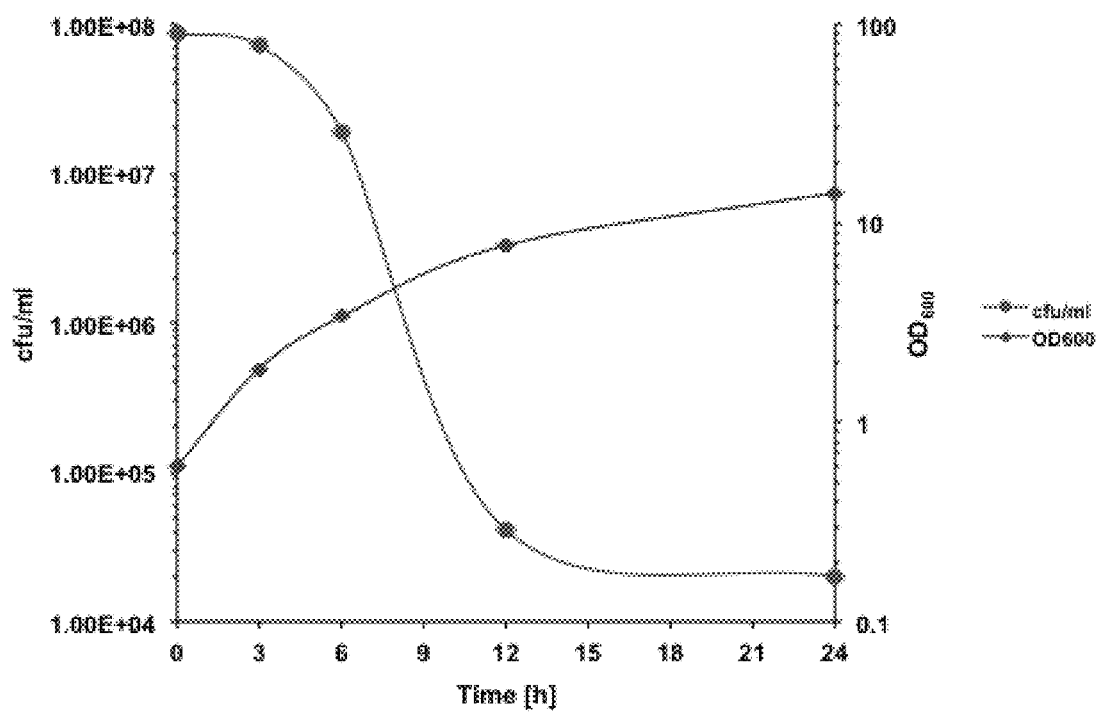
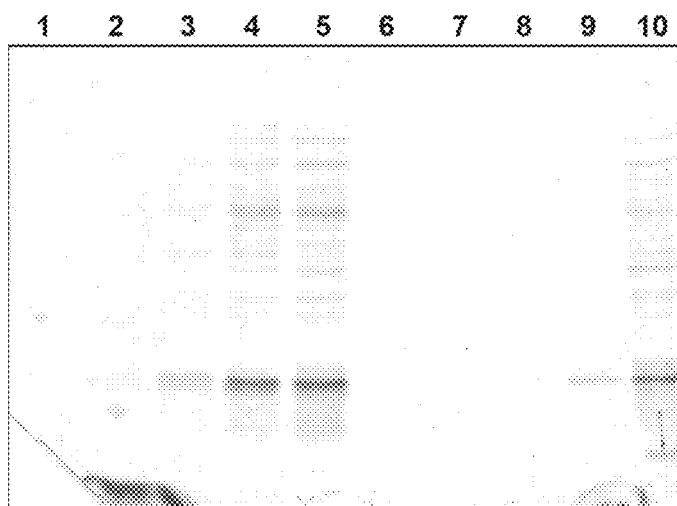
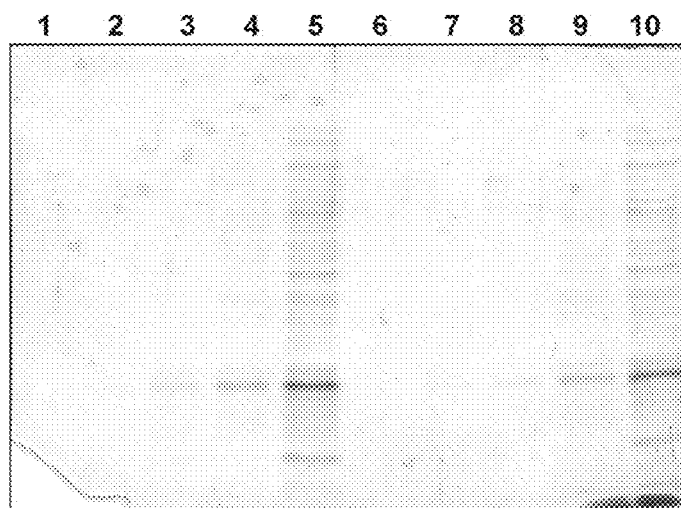


FIG. 50



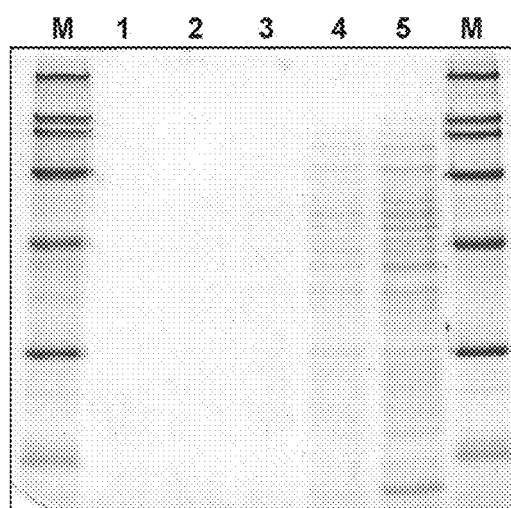
1. BW30270/pJexpress404:51150 -- uninduced
2. BW30270/pJexpress404:51150 - induced (3 h)
3. BW30270/pJexpress404:51150 - induced (6 h)
4. BW30270/pJexpress404:51150 - induced (12 h)
5. BW30270/pJexpress404:51150 - induced (24 h)
6. KPM318/pJexpress404:51150 - uninduced
7. KPM318/pJexpress404:51150 - induced (3 h)
8. KPM318/pJexpress404:51150 - induced (6 h)
9. KPM318/pJexpress404:51150 - induced (12 h)
10. KPM318/pJexpress404:51150 - induced (24 h)

FIG. 51



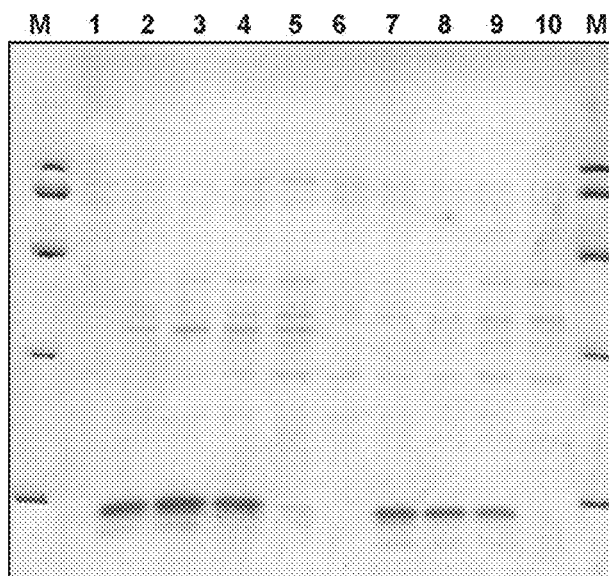
1. KPM318-9/pJexpress404:51150 - uninduced
2. KPM318-9/pJexpress404:51150 - induced (3 h)
3. KPM318-9/pJexpress404:51150 - induced (6 h)
4. KPM318-9/pJexpress404:51150 - induced (12 h)
5. KPM318-9/pJexpress404:51150 - induced (24 h)
6. KPM318-10/pJexpress404:51150 - uninduced
7. KPM318-10/pJexpress404:51150 - induced (3 h)
8. KPM318-10/pJexpress404:51150 - induced (6 h)
9. KPM318-10/pJexpress404:51150 - induced (12 h)
10. KPM318-10/pJexpress404:51150 - induced (24 h)

FIG. 52



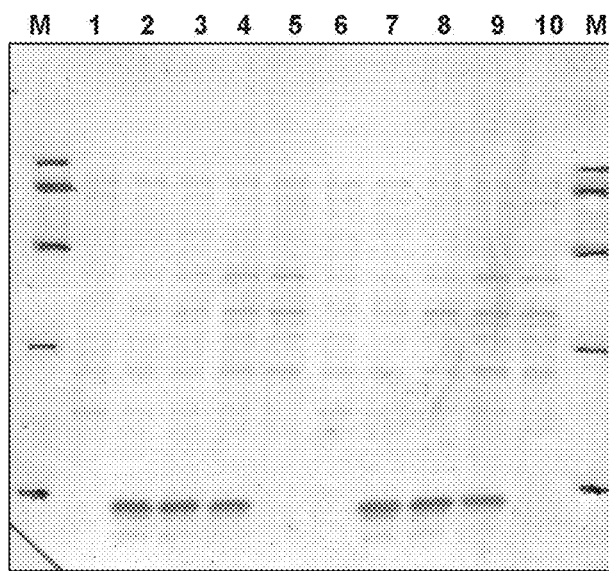
1. KPM318-19/pJexpress404:51150 – uninduced
2. KPM318-19/pJexpress404:51150 - induced (3 h)
3. KPM318-19/pJexpress404:51150 - induced (6 h)
4. KPM318-19/pJexpress404:51150 - induced (12 h)
5. KPM318-19/pJexpress404:51150 - induced (24 h)

FIG. 53



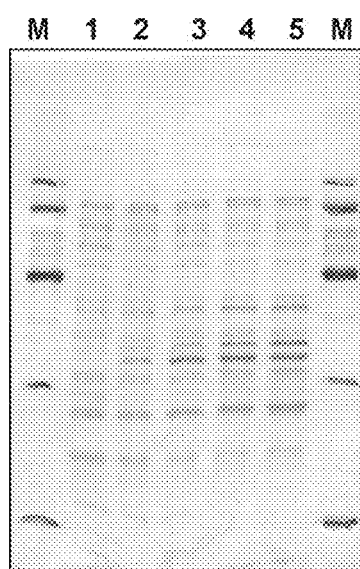
1. BW30270/pJexpress404:51149 - uninduced
2. BW30270/pJexpress404:51149 - induced (3 h)
3. BW30270/pJexpress404:51149 - induced (6 h)
4. BW30270/pJexpress404:51149 - induced (12 h)
5. BW30270/pJexpress404:51149 - induced (24 h)
6. KPM318/pJexpress404:51149 - uninduced
7. KPM318/pJexpress404:51149 - induced (3 h)
8. KPM318/pJexpress404:51149 - induced (6 h)
9. KPM318/pJexpress404:51149 - induced (12 h)
10. KPM318/pJexpress404:51149 - induced (24 h)

FIG. 54



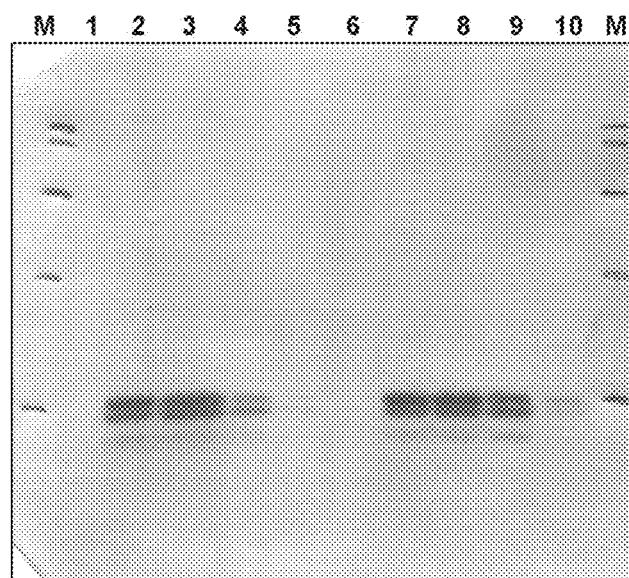
1. KPM318-9/pJexpress404:51149 - uninduced
2. KPM318-9/pJexpress404:51149 - induced (3 h)
3. KPM318-9/pJexpress404:51149 - induced (6 h)
4. KPM318-9/pJexpress404:51149 - induced (12 h)
5. KPM318-9/pJexpress404:51149 - induced (24 h)
6. KPM318-10/pJexpress404:51149 - uninduced
7. KPM318-10/pJexpress404:51149 - induced (3 h)
8. KPM318-10/pJexpress404:51149 - induced (6 h)
9. KPM318-10/pJexpress404:51149 - induced (12 h)
10. KPM318-10/pJexpress404:51149 - induced (24 h)

FIG. 55



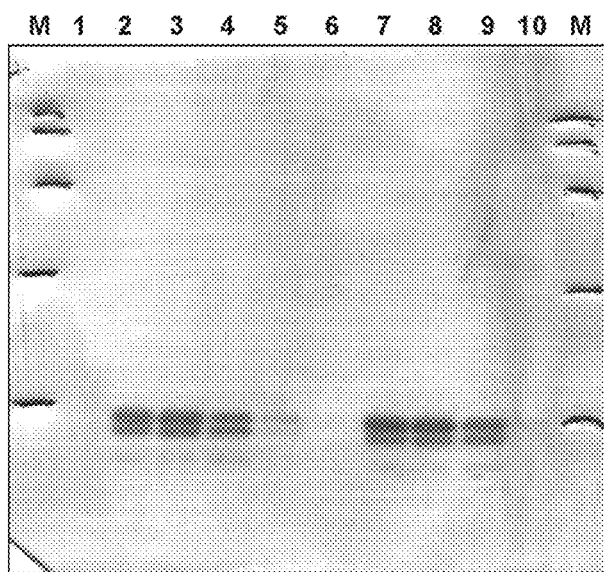
1. KPM318-19/pJexpress404:51149 – uninduced
2. KPM318-19/pJexpress404:51149 - induced (3 h)
3. KPM318-19/pJexpress404:51149 - induced (6 h)
4. KPM318-19/pJexpress404:51149 - induced (12 h)
5. KPM318-19/pJexpress404:51149 - induced (24 h)

FIG. 56



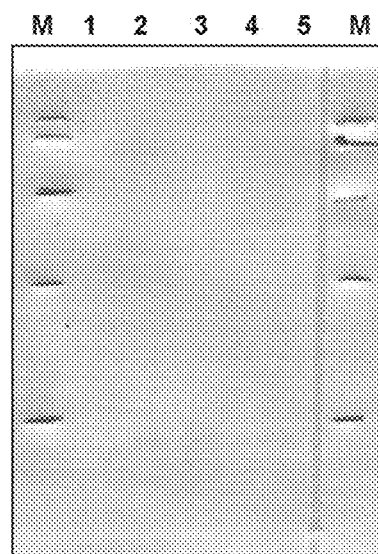
1. BW30270/pJexpress404:51150 - uninduced
2. BW30270/pJexpress404:51150 - induced (3 h)
3. BW30270/pJexpress404:51150 - induced (6 h)
4. BW30270/pJexpress404:51150 - induced (12 h)
5. BW30270/pJexpress404:51150 - induced (24 h)
6. KPM318/pJexpress404:51150 - uninduced
7. KPM318/pJexpress404:51150 - induced (3 h)
8. KPM318/pJexpress404:51150 - induced (6 h)
9. KPM318/pJexpress404:51150 - induced (12 h)
10. KPM318/pJexpress404:51150 - induced (24 h)

FIG. 57



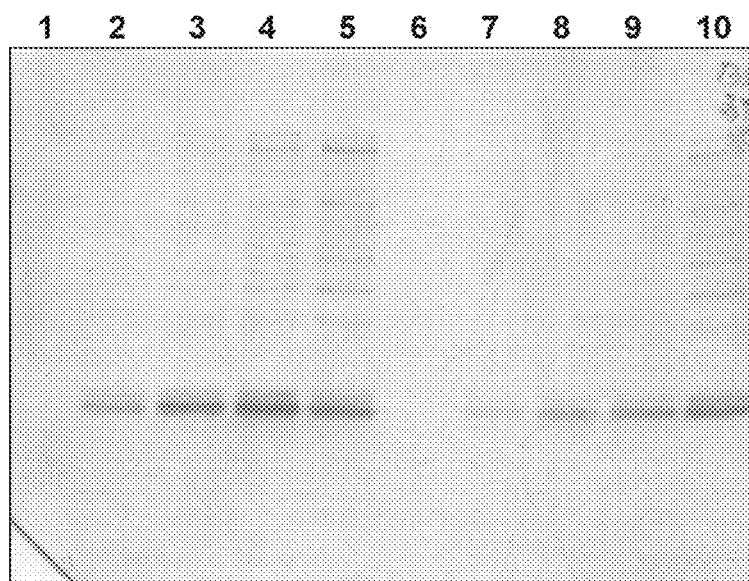
1. KPM318-9/pJexpress404:51150 - uninduced
2. KPM318-9/pJexpress404:51150 - induced (3 h)
3. KPM318-9/pJexpress404:51150 - induced (6 h)
4. KPM318-9/pJexpress404:51150 - induced (12 h)
5. KPM318-9/pJexpress404:51150 - induced (24 h)
6. KPM318-10/pJexpress404:51150 - uninduced
7. KPM318-10/pJexpress404:51150 - induced (3 h)
8. KPM318-10/pJexpress404:51150 - induced (6 h)
9. KPM318-10/pJexpress404:51150 - induced (12 h)
10. KPM318-10/pJexpress404:51150 - induced (24 h)

FIG. 58



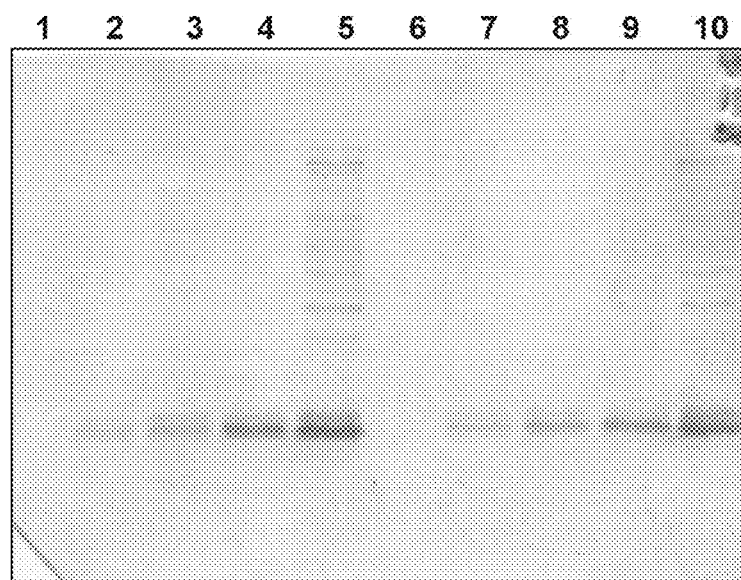
1. KPM318-19/pJexpress404:51150 – uninduced
2. KPM318-19/pJexpress404:51150 - induced (3 h)
3. KPM318-19/pJexpress404:51150 - induced (6 h)
4. KPM318-19/pJexpress404:51150 - induced (12 h)
5. KPM318-19/pJexpress404:51150 - induced (24 h)

FIG. 59



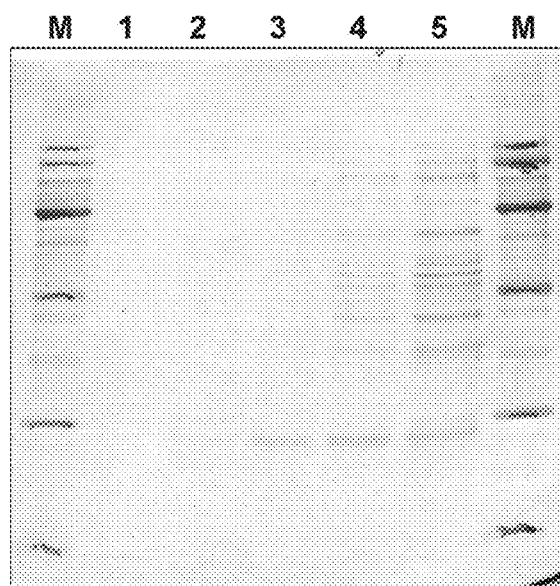
1. BW30270/pJexpress404:51150 – uninduced
2. BW30270/pJexpress404:51150 - induced (3 h)
3. BW30270/pJexpress404:51150 - induced (6 h)
4. BW30270/pJexpress404:51150 - induced (12 h)
5. BW30270/pJexpress404:51150 - induced (24 h)
6. KPM318/pJexpress404:51150 - uninduced
7. KPM318/pJexpress404:51150 - induced (3 h)
8. KPM318/pJexpress404:51150 - induced (6 h)
9. KPM318/pJexpress404:51150 - induced (12 h)
10. KPM318/pJexpress404:51150 - induced (24 h)

FIG. 60



1. KPM318-9/pJexpress404:51150 - uninduced
2. KPM318-9/pJexpress404:51150 - induced (3 h)
3. KPM318-9/pJexpress404:51150 - induced (6 h)
4. KPM318-9/pJexpress404:51150 - induced (12 h)
5. KPM318-9/pJexpress404:51150 - induced (24 h)
6. KPM318-10/pJexpress404:51150 - uninduced
7. KPM318-10/pJexpress404:51150 - induced (3 h)
8. KPM318-10/pJexpress404:51150 - induced (6 h)
9. KPM318-10/pJexpress404:51150 - induced (12 h)
10. KPM318-10/pJexpress404:51150 - induced (24 h)

FIG. 61



1. KPM318-19/pJexpress404:51150 – uninduced
2. KPM318-19/pJexpress404:51150 - induced (3 h)
3. KPM318-19/pJexpress404:51150 - induced (6 h)
4. KPM318-19/pJexpress404:51150 - induced (12 h)
5. KPM318-19/pJexpress404:51150 - induced (24 h)

FIG. 62

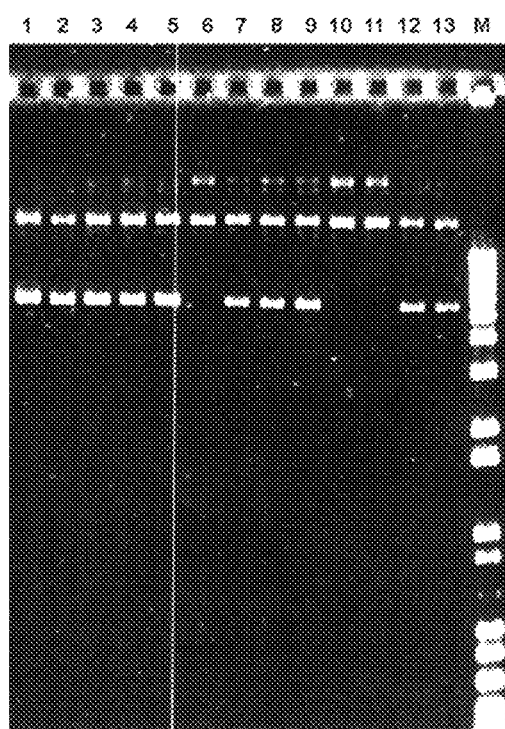


FIG. 63

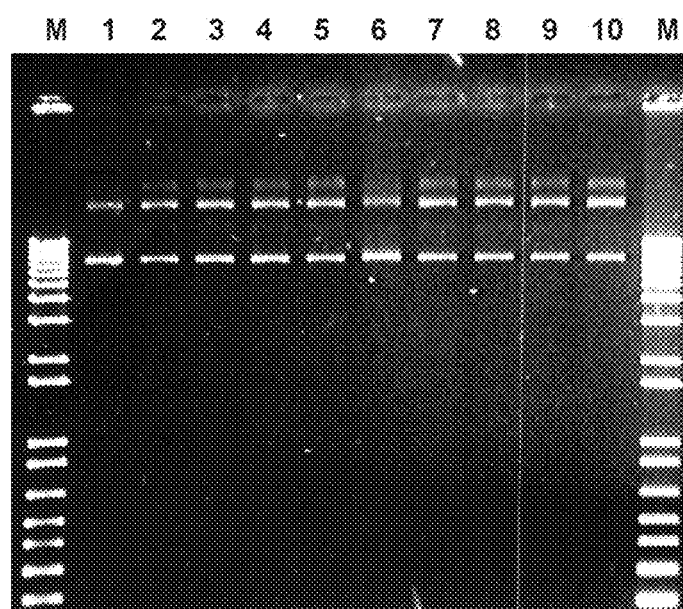


FIG. 64

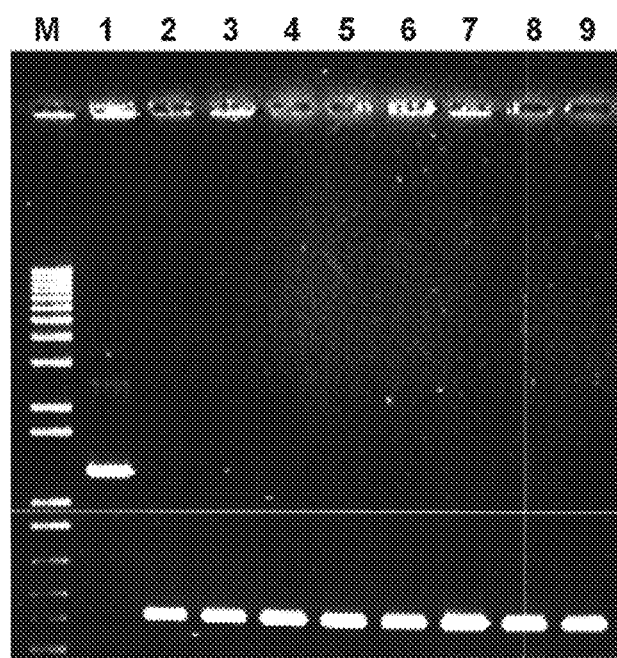


FIG. 65

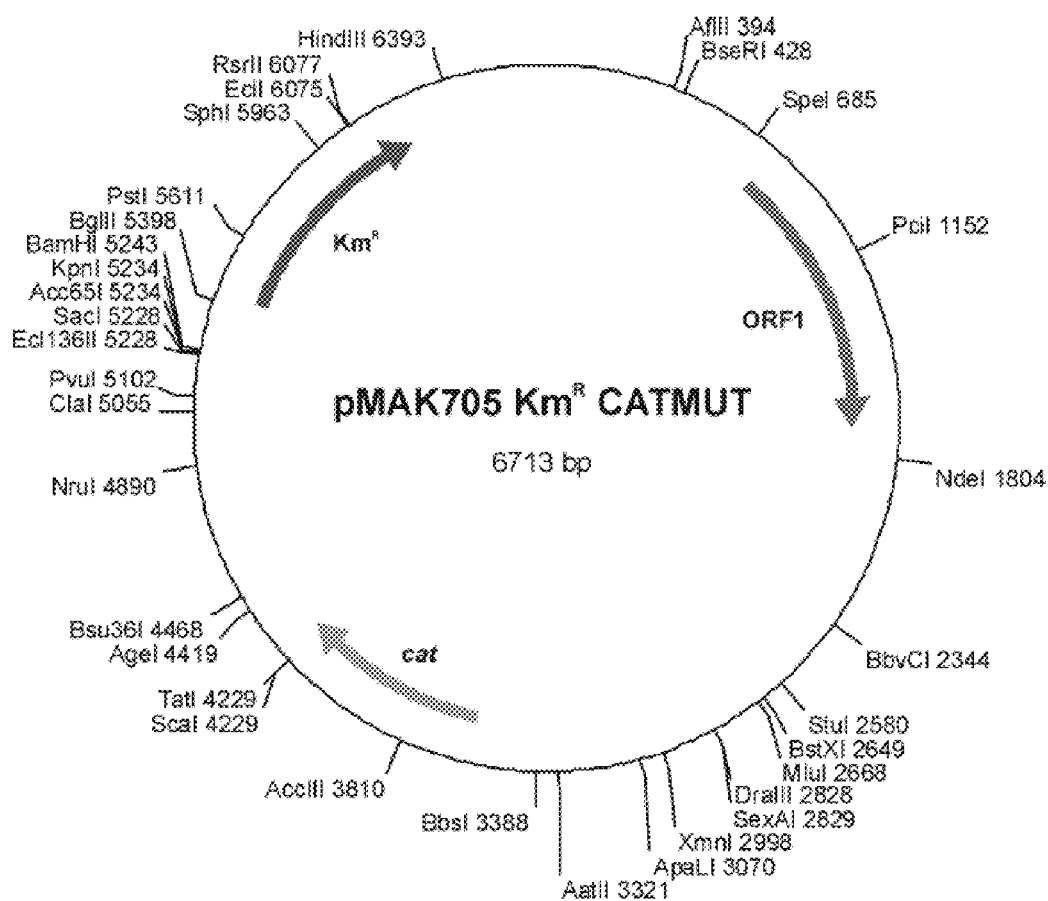
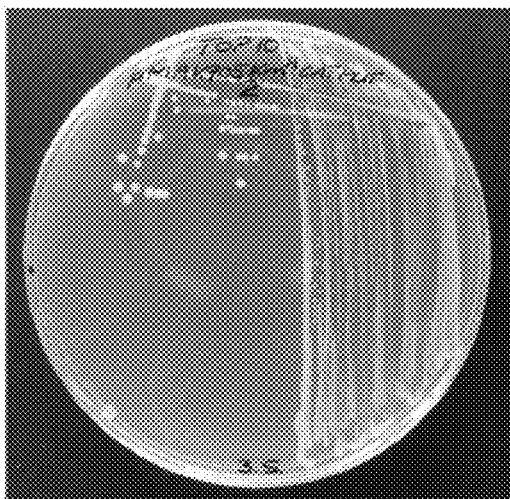
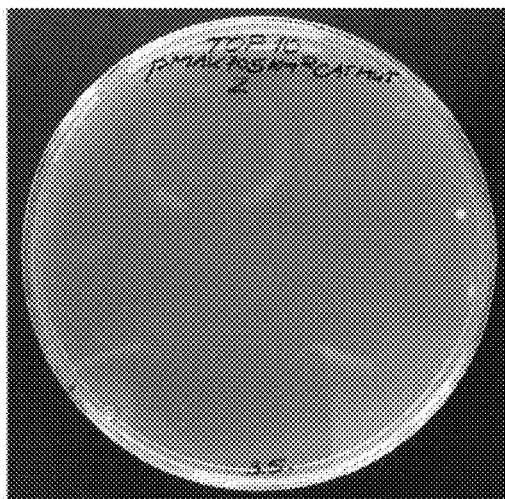


FIG. 66

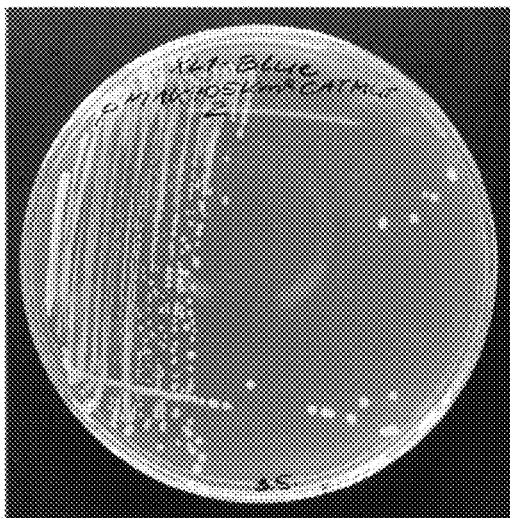
E. coli TOP10/pMAK705 Km^r CATMUT
LB + 30 µg/ml kanamycin



E. coli TOP10/pMAK705 Km^r CATMUT
LB + 30 µg/ml kanamycin + 15 µg/ml chloramphenicol



E. coli XL1-Blue/pMAK705 Km^r CATMUT
LB + 30 µg/ml kanamycin



E. coli XL1-Blue/pMAK705 Km^r CATMUT
LB + 30 µg/ml kanamycin + 15 µg/ml chloramphenicol

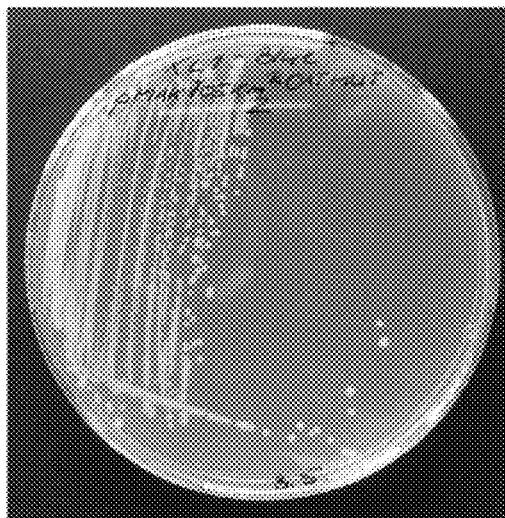


FIG. 67

Table 1. Examples of *E. coli* strains constructed.

Strain	Description
KPM274	KPM22 Δ <i>eptA</i> ::Km ⁺ ; Δ <i>eptA</i> ::Km ⁺ donor strain
KPM279	KPM22 Δ <i>lpxL</i> ::Km ⁺ ; Δ <i>lpxL</i> ::Km ⁺ donor strain
KPM280	KPM22 Δ <i>lpxM</i> ::Km ⁺ ; Δ <i>lpxM</i> ::Km ⁺ donor strain
KPM281	KPM22 Δ <i>lpxL</i>
KPM282	KPM22 Δ <i>lpxM</i>
KPM288	KPM22 L11 Δ <i>lpxL</i> ::Km ⁺
KPM290	KPM22 L11 Δ <i>lpxL</i> ::Km ⁺
KPM296	KPM22 L11 Δ <i>lpxL</i>
KPM296-6	42°C-resistant derivative of KPM296
KPM300	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i> ::Km ⁺
KPM303	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i>
BW30270 Δ <i>lpxP</i> ::Km ⁺	<i>E. coli</i> K-12 wild-type; Δ <i>lpxP</i> ::Km ⁺ donor strain
BW30270 Δ <i>pagP</i> ::Km ⁺	<i>E. coli</i> K-12 wild-type; Δ <i>pagP</i> ::Km ⁺ donor strain
KPM310	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i> Δ <i>pagP</i> ::Km ⁺
KPM312	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i> Δ <i>pagP</i>
KPM314	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i> Δ <i>pagP</i> Δ <i>lpxP</i> ::Km ⁺
KPM316	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i> Δ <i>pagP</i> Δ <i>lpxP</i>
KPM317	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i> Δ <i>pagP</i> Δ <i>lpxP</i> Δ <i>eptA</i> ::Km ⁺
KPM318	KPM22 L11 Δ <i>lpxL</i> Δ <i>lpxM</i> Δ <i>pagP</i> Δ <i>lpxP</i> Δ <i>eptA</i>

FIG. 68

Table 2. ESI FT-ICR MS peak list of glycoforms detected in *E. coli* KPM318.

Obs. Mass [m]	Calc. Mass [m]	Chemical Composition	Glycoform	
3544.4065	3544.3941	1* Gal 3* Glc 4* Hep 2* Kdo 4* P 1* P-EN	II	SEQID20
3556.4395	3556.3975	1* Gal 2* Glc 3* Hep 3* Kdo 4* P 1* P-EN 1* Rha	IV	SEQID21
3566.3895		1* Gal 3* Glc 4* Hep 2* Kdo 4* P 1* P-EN 1* Na	II	SEQID22
3578.3653		1* Gal 2* Glc 3* Hep 3* Kdo 4* P 1* P-EN 1* Rha 1* Na	IV	SEQID23
3624.4402	3624.3604	1* Gal 3* Glc 4* Hep 2* Kdo 5* P 1* P-EN	I	SEQID24
	3624.4651*GlcNAc	1* Gal 3* Glc 4* Hep 2* Kdo 4* P	II	SEQID25
3646.3195		1* Gal 3* Glc 4* Hep 2* Kdo 5* P 1* P-EN 1* Na	I	SEQID26
	1*GlcNAc	1* Gal 3* Glc 4* Hep 2* Kdo 5* P	II	SEQID27
3658.3357		1* Gal 2* Glc 3* Hep 3* Kdo 5* P 1* P-EN 1* Rha 1* Na	IV	SEQID28
3667.4007	3667.50721*GlcNAc	1* Gal 3* Glc 4* Hep 2* Kdo 3* P 1* P-EN	II	SEQID29
	3704.43131*GlcNAc	1* Gal 3* Glc 4* Hep 2* Kdo 3* P	II	SEQID30
3748.3038	1*GlcNAc	1* Gal 3* Glc 4* Hep 2* Kdo 3* P	II	SEQID31
	3747.47351*GlcNAc	1* Gal 3* Glc 4* Hep 2* Kdo 4* P 1* P-EN	II	SEQID32
	3783.4987	1* Gal 2* Glc 3* Hep 3* Kdo 4* P 1* P-EN 1* Rha 1* HexA 1* Ara4N		SEQID33
	3797.3734	1* Gal 2* Glc 3* Hep 3* Kdo 5* P 1* P-EN 1* HexA 1* Ara4N		SEQID34
	3798.54261*GlcNAc	1* Gal 3* Glc 4* Hep 2* Kdo 5* P 1* P-EN 1* Ara4N		SEQID35

FIG. 69

Table 3. Optical density and cell number of the bacterial suspensions immediately before the induction with IPTG.

Strain	Optical density (OD ₆₀₀) immediately before the induction	Cell number (cfu/ml)
BW30270/pJexpress404:51149	0.519	N.D.
KPM318/pJexpress404:51149	0.540	N.D.
KPM318-9/pJexpress404:51149	0.603	4.7×10^7
KPM318-10/pJexpress404:51149	0.566	9.2×10^7
KPM318-19/pJexpress404:51149	0.539	1.3×10^8
BW30270/pJexpress404:51150	0.555	8.0×10^5
KPM318/pJexpress404:51150	0.548	6.4×10^7
KPM318-9/pJexpress404:51150	0.600	7.1×10^7
KPM318-10/pJexpress404:51150	0.601	8.5×10^7
KPM318-19/pJexpress404:51150	0.633	1.5×10^8

FIG. 70

Table 4. Optical density and cell number of the bacterial suspensions after 3 hr of induction.

Strain	Optical density (OD ₆₀₀) 3 h post-induction	Cell number (cfu/ml)
BW30270/pJexpress404:51149	2.66	N.D.
KPM318/pJexpress404:51149	2.89	N.D.
KPM318-9/pJexpress404:51149	2.76	7.4×10^8
KPM318-10/pJexpress404:51149	2.73	7.8×10^8
KPM318-19/pJexpress404:51149	1.73	7.8×10^8
BW30270/pJexpress404:51150	1.73	1.0×10^8
KPM318/pJexpress404:51150	2.04	3.9×10^7
KPM318-9/pJexpress404:51150	1.93	4.4×10^7
KPM318-10/pJexpress404:51150	1.86	7.2×10^7
KPM318-19/pJexpress404:51150	1.49	1.0×10^8

FIG. 71

Table 5. Optical density and cell number of the bacterial suspensions after 6 hr of induction.

Strain	Optical density (OD ₆₀₀) 6 hr post-induction	Cell number (cfu/ml)
BW30270/pJexpress404:51149	4.85	N.D.
KPM318/pJexpress404:51149	4.99	N.D.
KPM318-9/pJexpress404:51149	4.77	9.6×10^8
KPM318-10/pJexpress404:51149	4.61	2.0×10^9
KPM318-19/pJexpress404:51149	3.59	2.7×10^8
BW30270/pJexpress404:51150	2.57	3.5×10^7
KPM318/pJexpress404:51150	3.32	2.1×10^7
KPM318-9/pJexpress404:51150	3.42	2.3×10^8
KPM318-10/pJexpress404:51150	3.39	1.9×10^7
KPM318-19/pJexpress404:51150	2.38	2.3×10^8

FIG. 72

Table 6. Optical density and cell number of the bacterial suspensions after 12 hr of induction.

Strain	Optical density (OD ₆₀₀) 12 hr post-induction	Cell number (cfu/ml)
BW30270/pJexpress404:51149	8.73	N.D.
KPM318/pJexpress404:51149	8.74	N.D.
KPM318-9/pJexpress404:51149	9.08	6.9×10^8
KPM318-10/pJexpress404:51149	9.10	8.7×10^8
KPM318-19/pJexpress404:51149	6.15	2.2×10^7
BW30270/pJexpress404:51150	6.80	1.0×10^7
KPM318/pJexpress404:51150	7.59	1.0×10^5
KPM318-9/pJexpress404:51150	7.44	3.1×10^4
KPM318-10/pJexpress404:51150	7.75	4.1×10^4
KPM318-19/pJexpress404:51150	4.63	5.8×10^7

FIG. 73

Table 7. Optical density and cell number of the bacterial suspensions after 24 hr of induction.

Strain	Optical density (OD ₆₀₀) 24 hr post-induction	Cell number (cfu/ml)
BW30270/pJexpress404:51149	12.95	N.D.
KPM318/pJexpress404:51149	11.85	N.D.
KPM318-9/pJexpress404:51149	10.50	3.0×10^8
KPM318-10/pJexpress404:51149	10.90	to the 10^{-6} dilut.: -
KPM318-19/pJexpress404:51149	7.75	1.0×10^7
BW30270/pJexpress404:51150	10.00	5.0×10^5
KPM318/pJexpress404:51150	13.75	4.2×10^4
KPM318-9/pJexpress404:51150	12.30	2.4×10^4
KPM318-10/pJexpress404:51150	14.20	2.0×10^4
KPM318-19/pJexpress404:51150	7.50	2.0×10^5

FIG. 74

Table 8. Determination of the amount of culture media obtained from cells immediately before the induction with IPTG.

Strain	Optical density (OD ₆₀₀) immediately before the induction	Culture medium (μl)
BW30270/pJexpress404:51150	0.555	9.9
KPM318/pJexpress404:51150	0.548	10.0
KPM318-9/pJexpress404:51150	0.600	9.1
KPM318-10/pJexpress404:51150	0.601	9.1
KPM318-19/pJexpress404:51150	0.633	8.7

FIG. 75

Table 9. Determination of the amount of culture media obtained from cells after 3 hr of induction.

Strain	Optical density (OD ₆₀₀) 3 hr post-induction	Culture medium (μl)
BW30270/pJexpress404:51150	1.73	8.6
KPM318/pJexpress404:51150	2.04	7.3
KPM318-9/pJexpress404:51150	1.93	7.7
KPM318-10/pJexpress404:51150	1.86	8.0
KPM318-19/pJexpress404:51150	1.49	10.0

FIG. 76

Table 10. Determination of the amount of culture media obtained from cells after 6 hr of induction.

Strain	Optical density (OD ₆₀₀) 6 hr post-induction	Culture medium (μl)
BW30270/pJexpress404:51150	2.57	9.3
KPM318/pJexpress404:51150	3.32	7.2
KPM318-9/pJexpress404:51150	3.42	7.0
KPM318-10/pJexpress404:51150	3.39	7.0
KPM318-19/pJexpress404:51150	2.38	10.0

FIG. 77

Table 11. Determination of the amount of culture media obtained from cells after 12 hr of induction.

Strain	Optical density (OD ₆₀₀) 12 hr post-induction	Culture medium (μl)
BW30270/pJexpress404:51150	6.80	6.8
KPM318/pJexpress404:51150	7.59	6.1
KPM318-9/pJexpress404:51150	7.44	6.2
KPM318-10/pJexpress404:51150	7.75	6.0
KPM318-19/pJexpress404:51150	4.63	10.0

FIG. 78

Table 12. Determination of the amount of culture media obtained from cells after 24 hr of induction.

Strain	Optical density (OD ₆₀₀) 24 hr post-induction	Culture medium (μl)
BW30270/pJexpress404:51150	10.00	7.5
KPM318/pJexpress404:51150	13.75	5.4
KPM318-9/pJexpress404:51150	12.30	6.1
KPM318-10/pJexpress404:51150	14.20	5.3
KPM318-19/pJexpress404:51150	7.50	10.0

FIG. 79

Table 13. Number of electrocompetent cells.

Strain	Cell number (cfu/ml)
BW30270	7.3×10^8
KPM318 (LB)	4×10^9
KPM318 (LB A5P/G6P)	1.1×10^9

FIG. 80

Table 14. Transformation efficiencies for *E. coli* strains BW30270, KPM318 (LB) and KPM318 (LB A5P/G6P).

Strain	Transformation efficiency (cfu/ μ g pMAL-c2 DNA)
BW30270	1.06×10^7
KPM318 (LB)	3.64×10^6
KPM318 (LB A5P/G6P)	2.51×10^7

FIG. 81

Table 15. Transformation efficiencies for *E. coli* strains KPM318-9, KPM318-10, KPM318-19, and KPM318-23.

Strain	Transformation efficiency (cfu/μg pMAL-c2 DNA)	Transformation efficiency (cfu/μg pMAL-p2 DNA)
KPM318-9	3.44×10^7	7.12×10^7
KPM318-10	2.33×10^7	2.78×10^7
KPM318-19	1.29×10^8	1.40×10^8
KPM318-23	1.08×10^4	8.20×10^3

FIG. 82

Table 16. Yields of plasmids pMAL-c2 and pMAL-p2 isolated from *E. coli* strains BW30270, KPM318, KPM318-9, KPM318-10, KPM318-19, and KPM318-23.

Strain	Yield of pMAL-c2 (μg DNA/5 ml culture)	Yield of pMAL-p2 (μg DNA/5 ml culture)
BW30270	1.36	3.04
KPM318	0.76	0.92
KPM318-9	1.6	1.44
KPM318-10	1.28	1.2
KPM318-19	0.88	0.92
KPM318-23	0.48	0.28

FIG. 83

Table 17. Calculation of the amount of the recipient (BW30270 and KPM318) to add to 500 μ l of the donor (JC19022 F'121 Tn10).

Strain	OD₆₀₀	Amount of the recipient in μl to add to 500 μl of the donor
JC19022 F'121 Tn10 (25 μ l)	0.019	-
JC19022 F'121 Tn10 (50 μ l)	0.035	-
JC19022 F'121 Tn10 (100 μ l)	0.07	-
JC19022 F'121 Tn10 (200 μ l)	0.111	-
BW30270 (25 μ l)	0.264	210 μ l
BW30270 (50 μ l)	0.432	-
BW30270 (100 μ l)	0.697	-
BW30270 (200 μ l)	1.008	-
KPM318 (25 μ l)	0.055	-
KPM318 (50 μ l)	0.109	509 μ l
KPM318 (100 μ l)	0.212	-
KPM318 (200 μ l)	0.372	-

FIG. 84

Table 18. Calculation of the amount of the recipient (KPM318-9, KPM318-10, KPM318-19, and KPM318-23) to add to 500 μ l of the donor (JC19022 F'121 Tn10).

Strain	OD₆₀₀	Amount of the recipient in μl to add to 500 μl of the donor
JC19022 F'121 Tn10 (25 μ l)	0.035	-
JC19022 F'121 Tn10 (50 μ l)	0.048	-
JC19022 F'121 Tn10 (100 μ l)	0.105	-
JC19022 F'121 Tn10 (200 μ l)	0.163	-
KPM318-9 (25 μ l)	0.117	449 μ l
KPM318-9 (50 μ l)	0.226	-
KPM318-9 (100 μ l)	0.352	-
KPM318-9 (200 μ l)	0.654	-
KPM318-10 (25 μ l)	0.134	392 μ l
KPM318-10 (50 μ l)	0.244	-
KPM318-10 (100 μ l)	0.446	-
KPM318-10 (200 μ l)	0.710	-
KPM318-19 (25 μ l)	0.029	-
KPM318-19 (50 μ l)	0.068	-
KPM318-19 (100 μ l)	0.131	401 μ l
KPM318-19 (200 μ l)	0.245	-
KPM318-23 (25 μ l)	0.127	413 μ l
KPM318-23 (50 μ l)	0.241	-
KPM318-23 (100 μ l)	0.430	-
KPM318-23 (200 μ l)	0.737	-

FIG. 85

Table 19. Optical densities (OD₆₀₀) of the strains immediately before the M13KO7 infection.

Strain	OD ₆₀₀ immediately before the M13KO7 infection
BW30270 (control)	0.717
JC19022 (F'121 Tn10) - control	0.559
KPM318 (control)	0.344
BW30270 (F'121 Tn10)-1	0.581
BW30270 (F'121 Tn10)-2	0.574
BW30270 (F'121 Tn10)-3	0.600
BW30270 (F'121 Tn10)-4	0.623
KPM318 (F'121 Tn10)-4	0.410
KPM318 (F'121 Tn10)-6	0.178
KPM318 (F'121 Tn10)-7	0.174
KPM318 (F'121 Tn10)-8	0.157
KPM318-9 (F'121 Tn10)-1	0.128
KPM318-9 (F'121 Tn10)-2	0.246
KPM318-9 (F'121 Tn10)-3	0.098
KPM318-9 (F'121 Tn10)-4	0.261
KPM318-10 (F'121 Tn10)-1	0.111
KPM318-10 (F'121 Tn10)-3	0.289
KPM318-10 (F'121 Tn10)-4	0.166
KPM318-10 (F'121 Tn10)-5	0.406
KPM318-19 (F'121 Tn10)-6*	0.136
KPM318-23 (F'121 Tn10)-1	0.219
KPM318-23 (F'121 Tn10)-2	0.328
KPM318-23 (F'121 Tn10)-3	0.280
KPM318-23 (F'121 Tn10)-5	0.252

FIG. 86

Table 20. Number of kanamycin-resistant colonies following infection of potential F'121 Tn10 transconjugants with M13KO7 helper phage.

Strain	Number of kanamycin-resistant colonies (cfu/ml)
BW30270 (control)	0
JC19022 (F'121 Tn10) - control	2.8×10^8
KPM318 (control)	8.5×10^2
BW30270 (F'121 Tn10)-1	2.7×10^8
BW30270 (F'121 Tn10)-2	1.0×10^8
BW30270 (F'121 Tn10)-3	2.1×10^8
BW30270 (F'121 Tn10)-4	1.7×10^8
KPM318 (F'121 Tn10)-4	4.2×10^4
KPM318 (F'121 Tn10)-6	5.5×10^3
KPM318 (F'121 Tn10)-7	4.4×10^3
KPM318 (F'121 Tn10)-8	6.4×10^4
KPM318-9 (F'121 Tn10)-1	1.4×10^7
KPM318-9 (F'121 Tn10)-2	4.1×10^5
KPM318-9 (F'121 Tn10)-3	3.8×10^7
KPM318-9 (F'121 Tn10)-4	5.6×10^7
KPM318-10 (F'121 Tn10)-1	3.6×10^5
KPM318-10 (F'121 Tn10)-3	7.6×10^4
KPM318-10 (F'121 Tn10)-4	6.5×10^7
KPM318-10 (F'121 Tn10)-5	7.8×10^5
KPM318-19 (F'121 Tn10)-6	6.4×10^6
KPM318-23 (F'121 Tn10)-1	9.8×10^5
KPM318-23 (F'121 Tn10)-2	3.7×10^7
KPM318-23 (F'121 Tn10)-3	1.0×10^7
KPM318-23 (F'121 Tn10)-5	2.3×10^4

FIG. 87

Table 21: Sequences referred to in this application.

SEQ ID No.	Amino Acid Sequence
SEQID1	ATATGGATCCTTACATGGCGATAGCTAGACTGG
SEQID2	ATATAAGCTTGAAGAACTCCAGCATGAGATCC
SEQID3	GAGAAAAAATCACTGGATATACCTAGGTTGATATATCCCAATGGCA
SEQID4	CAGTACTGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATC
SEQID5	GTCGATAAGCTGATTACCGACGC
SEQID6	GTGAAACTATTTCGTCAGGCACTGG
SEQID7	CTACTGCGTATGCATTGCAG
SEQID8	TCGTAATCTTCTGCCGTAGC
SEQID9	ATGCATAACGACAAAGATCTCTCTACGTGGCAGACATTCGGCCGACTGTGGTCAACC ATTGCGCCTTTCAAAGCGGGTCTGATCGTGGCGGGCGTAGCGTTAATCCTCAACGCA GCCAGCGATACCTTCATGTTATCGCTCCTTAAGCCACTTCTTGATGATGGCTTTGGTA AAACAGATCGCTCCGTGCTGGTGGATGCCGCTGGTGGTGATCGGGCTGATGATT TTACGTGGTATCACCAGCTATGTCTCCAGCTACTGTATCTCCTGGGTATCAGGAAAG GTGGTAATGACCATGCGTCGCCGCCTGTTTGGTCACATGATGGGAATGCCAGTTTCA TTCTTTGACAAACAGTCAACGGGTACGCTGTTGTCACGTATTACCTACGATTCCGAAC AGGTTGCTTCTTCTTCCGGCGCACTGATTACTGTTGTGCGTGAAGGTGCGTCGA TCATCGGCCTGTTTCATCATGATGTTCTATTACAGTTGGCAACTGTCGATCATTTTGATT GTGCTGGCACCATTGTTTCGATTGCGATTGCGGTTGTATCGAAGCGTTTTTCGCAAC ATCAGTAAAAACATGCAGAACACCATGGGGCAGGTGACCACCAGCGCAGAACAAAT GCTGAAGGGCCACAAAGAAGTATTGATTTTCGGTGGTCAGGAAGTGGAAACGAAACG CTTTGATAAAGTCAGCAACCGAATGCGTCTTCAGGGGATGAAAATGGTTTCAGCCTC TTCCATCTCTGATCCGATCATTACAGCTGATCGCCTCTTTGGCGCTGGCGTTTGTCTG TATGCGGCGAGCTTCCCAAGTGTATGGATAGCCTGACTGCCGGTACGATTACCGTT GTTTTCTCTTCAATGATTGCACTGATGCGTCCGCTGAAATCGCTGACCAACGTTAACG CCCAGTTCCAGCGCGGTATGGCGGCTTGTGACAGCTGTTTACCATTCTGGACAGTG AGCAGGAGAAAGATGAAGGTAAGCGCGTGATCGAGCGTGCGACTGGCGACGTGGA ATTCCGCAATGTCACCTTTACTTATCCGGGACGTGACGTACCTGCATTGCGTAACATC AACCTGAAAATTCCGGCAGGGAAGACGGTTGCTCTGGTTGGACGCTCTGGTTCCGG TAAATCAACCATCGCCAGCCTGATCACGCGTTTTTACGATATTGATGAAGGCGAAATC CTGATGGATGGTCACGATCTGCGCGAGTATACCCTGGCGTCGTTACGTAACCAGGTT GCTCTGGTGTGCGAGAATGTCCATCTGTTTAACGATACGGTTGCTAACAACATTGCTT ACGCACGGACTGAACAGTACAGCCGTGAGCAAATTGAAGAAGCGGGCGCTATGGCC TACGCCATGGACTTCATCAATAAGATGGATAACGGTCTCGATACAGTGATTGGTGAAA ACGGCGTGCTGCTCTCTGGCGGTGACGCTGACGCTATTGCTATCGCTCGAGCCTTG TTGCGTGATAGCCCGATTCTGATTCTGGACGAAGCTACCTCGGCTCTGGATACCGAA TCCGAACGTGCGATTACAGCGGCACTGGATGAGTTGCAGAAAAACCGTACCTCTCTG GTGATTGCCACCGCTTGTCTACCATTTGAAAAGGCAGACGAAATCGTGCTCGTCGAG GATGGTGTGATTGTGGAACGCGGTACGCATAACGATTGCTTGAGCACCAGCGGCGTT TACGCGCAACTTCACAAAATGCAGTTTGGCCAATGA

FIG. 88

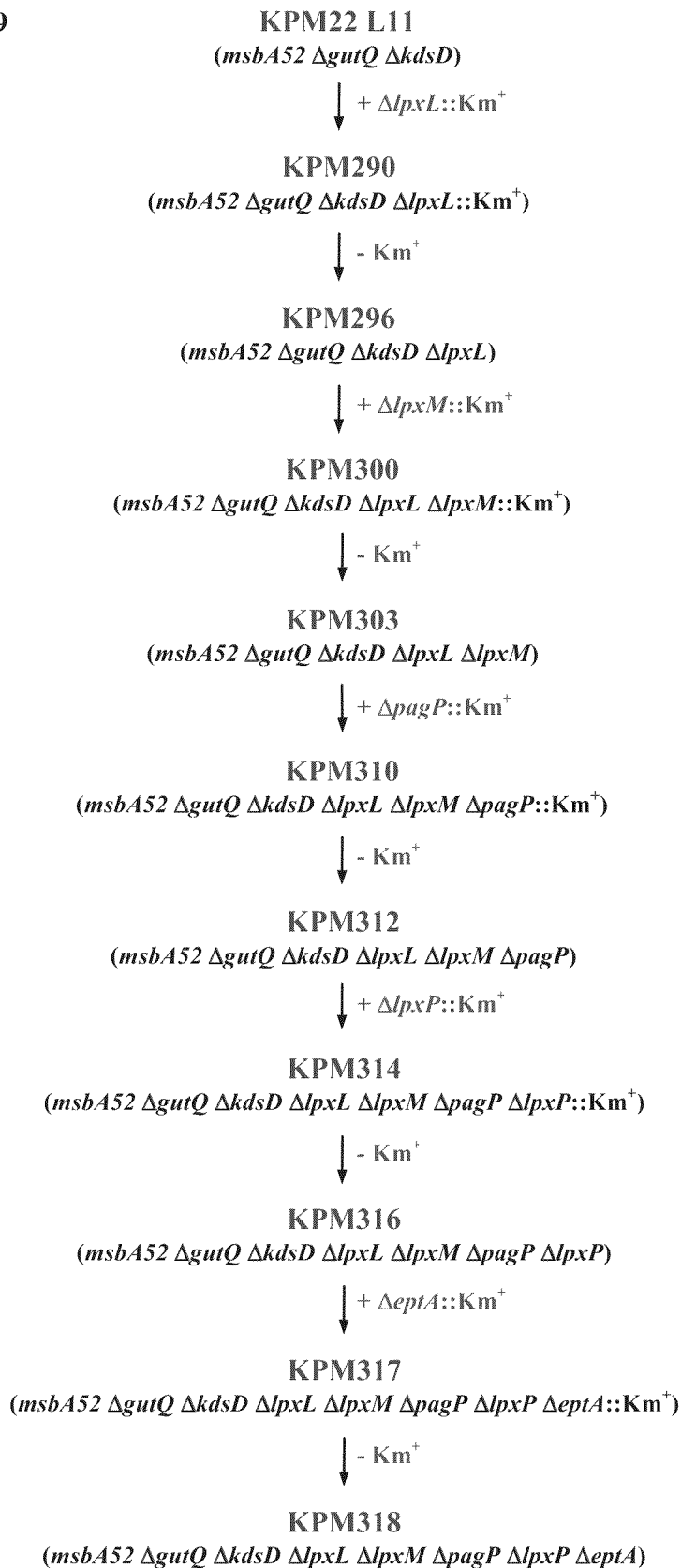
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SEQID11	TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCGG AATAGGAACTAAGGAGGATATTCATATGC
SEQID12	CTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAATATAGGAA CTTCGAAGCAGCTCCAGCCTACACC
SEQID13	GTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAATATAGGAA CTTCGAAGCAGCTCCAGCCTACACC
SEQID14	AGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCGG AATAGGAACTAAGGAGGATATTCATATGG
SEQID15	TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCGG AATAGGAACTAAGGAGGATATTCATATGC
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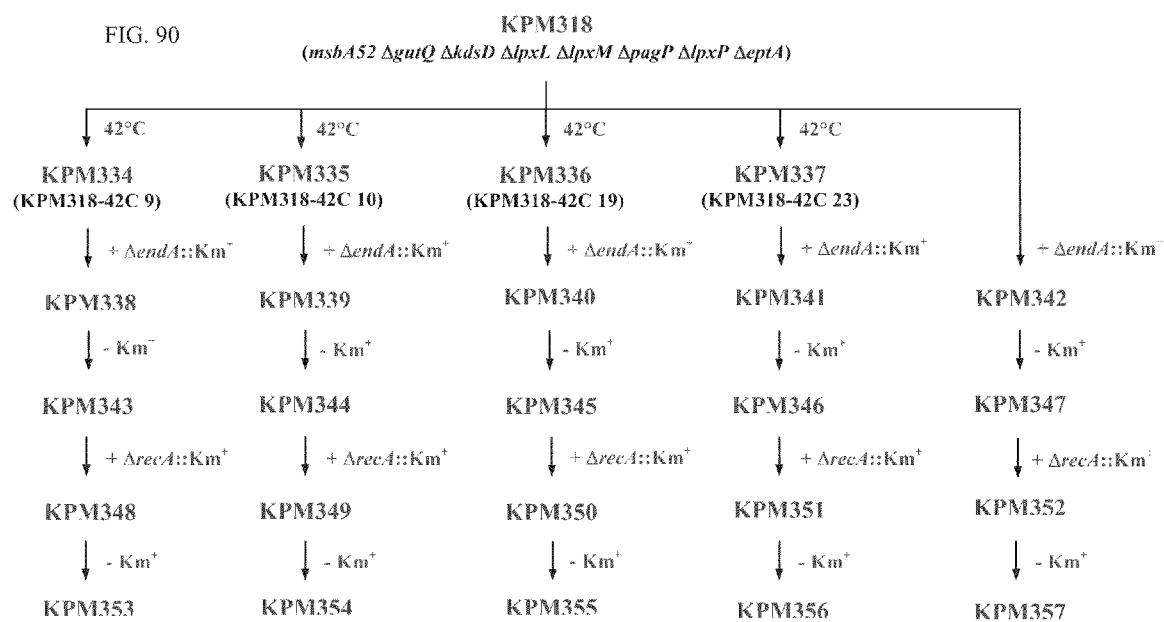
FIG. 88 cont.

SEQID17	CGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCGG AATAGGAAGGTCGACGGATCCCCGGAATG
SEQID18	TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCGG AATAGGAACTAAGGAGGATATTCATATGC
SEQID19	CTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTATAGGAA CTTCGAAGCAGCTCCAGCCTACACC
SEQID20	GTATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTATAGGAA CTTCGAAGCAGCTCCAGCCTACACG
SEQID21	AGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCGG AATAGGAACTAAGGAGGATATTCATATGG
SEQID22	TGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATACTTTCTAGAGAATAGGAACTTCGG AATAGGAACTAAGGAGGATATTCATATGC
SEQID23	TCATATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCCTATTCTCTAGAAAGTATAGG AACTTCGAAGCAGCTCCAGCCTACACC

FIG. 88 cont.

FIG. 89





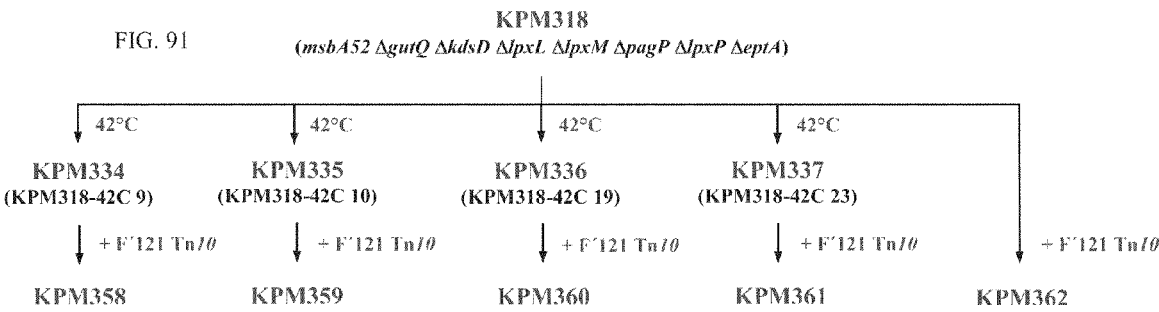


FIG. 92a

HEK-Blue™-hTLR4 Cells

SEAP Reporter 293 cells expressing the human TLR4 gene

Catalog # hkb-hlr4

For research use only

Version # 11C08-MM

PRODUCT INFORMATION

Contents and Storage

• 1 vial of HEK-Blue™-hTLR4 Cells (5-7 x 10⁶ cells) in Freezing Medium
IMPORTANT: Cells are shipped frozen. If cells are not frozen upon arrival, contact InvivoGen immediately.

• 1 vial 250X HEK-Blue™ Selection. A solution containing several selection antibiotics. HEK-Blue™ Selection can be stored at 4°C for 6 months or at -20°C for 12 months.

• 1 ml Normocin™ (50 mg/ml). Normocin™ is a formulation of three antibiotics active against mycoplasmas, bacteria and fungi. Store at -20°C. Product is stable for 18 months when stored at -20°C.

• 1 pouch of QUANTI-Blue™, alkaline phosphatase detection reagent. Store pouch at room temperature. Store reconstituted QUANTI-Blue™ at 4°C for 2 weeks.

PRODUCT DESCRIPTION

HEK-Blue™-hTLR4 Cells are designed for studying the stimulation of human TLR4 (hTLR4) by monitoring the activation of NF-κB. TLR4, the first human TLR identified, is the receptor for bacterial lipopolysaccharide (LPS) and lipid A, its toxic moiety. However, TLR4 alone is not sufficient to confer LPS responsiveness. TLR4 requires MD-2, a secreted molecule, to functionally interact with LPS¹. Furthermore, a third protein, called CD14, was shown to participate in LPS signaling, leading to the activation of NF-κB and the production of proinflammatory cytokines².

HEK-Blue™-hTLR4 Cells were obtained by co-transfection of the hTLR4, MD-2/CD14 co-receptor genes and a secreted embryonic alkaline phosphatase (SEAP) reporter gene into HEK293 cells. The SEAP reporter gene is placed under the control of an IL-12 p40 minimal promoter fused to five NF-κB and AP-1 binding sites. Stimulation with a TLR4 ligand activates NF-κB and AP-1 which induces the production of SEAP. Levels of SEAP can be easily determined with HEK-Blue™ Detection or QUANTI-Blue™, detection media that turn purple/blue in the presence of alkaline phosphatase. HEK-Blue™ Detection is designed for high-throughput detection of SEAP, while QUANTI-Blue™ is more sensitive and designed for the detection and quantification of SEAP.

HEK293 cells express endogenous levels of TLR3, TLR5 and NOD1.

NOTE: The parental cell line for HEK-Blue™-hTLR4 Cells is HEK-Blue™-Null2 Cells (SEAP reporter cells which do not express hTLR4).

1. Chow J, et al., 1999. Toll-like receptor-4 mediates lipopolysaccharide-induced signal transduction. *J Biol Chem* 274: 10669-92. 2. Shimazu R, et al., 1999. MD-2, a molecule that confers lipopolysaccharide responsiveness on Toll-like receptor 4. *J Exp Med*, 189(11): 1777-82. 3. Shuto T, et al., 2005. Membrane-anchored CD14 is required for LPS-induced TLR4 endocytosis in TLR4/MD-2/CD14 overexpressing CHO cells. *Biochem Biophys Res Commun* 338: 1402-9

Handling Cells Upon Arrival

We strongly recommend that you propagate the cells, using the provided procedure, as soon as possible. This will ensure the best cell viability and assay performance. Frozen cells may be placed in liquid nitrogen until you are ready to thaw and propagate them, however, this may reduce cell viability.

Product Warranty

InvivoGen warrants that cells shall be viable upon shipment from InvivoGen for a period of thirty days, provided they have been properly stored and handled during this period.

Cell Line Stability

Cells will undergo genotypic changes resulting in reduced responsiveness over time in normal cell culture conditions. Genetic instability is a biological phenomenon that occurs in all stably transfected cells. Therefore, it is critical to prepare an adequate number of frozen stocks at early passages.

HEK-Blue™-hTLR4 Cells should not be passaged more than 20 times to remain fully efficient. HEK-Blue™-hTLR4 Cells should be maintained in Growth Medium as described below in the presence of Normocin™ (100 µg/ml) and 1X HEK-Blue™ Selection. Antibiotic pressure with HEK-Blue™ Selection is required to maintain the plasmids coding hTLR4, MD-2/CD14 and SEAP.

Quality control

Expression of TLR4 and MD-2/CD14 genes was confirmed by RT-PCR. HEK-Blue™-hTLR4 Cells were stimulated by TLR4 agonists. As expected, TLR4 agonists induced the production of SEAP. These cells are guaranteed mycoplasma-free.

USE RESTRICTIONS

These cells are distributed for research purposes only.

This product is covered by a Limited Use License. By use of this product, the buyer agrees the terms and conditions of all applicable Limited Use Label Licenses. For non-research use, such as screening, quality control or clinical development, contact info@invivogen.com

Required Cell Culture Medium

• Growth Medium: DMEM, 4.5 g/l glucose, 10% (v/v) fetal bovine serum, 50 U/ml penicillin, 50 µg/ml streptomycin, 100 µg/ml Normocin™, 2 mM L-glutamine

• Freezing Medium: DMEM, 4.5 g/l glucose, 20% (v/v) fetal bovine serum, 50 U/ml penicillin, 50 µg/ml streptomycin, 100 µg/ml Normocin™, 2 mM L-glutamine, 10% (v/v) DMSO

• Test Medium (for use with QUANTI-Blue™): DMEM, 4.5 g/l glucose, 50 U/ml penicillin, 50 µg/ml streptomycin, 100 µg/ml Normocin™, 2 mM L-glutamine, 10% (v/v) heat-inactivated fetal bovine serum (30 min at 56°C)

TECHNICAL SUPPORT

Toll free (US): 888-457-5873

Outside US: (+1) 858-457-5873

Europe: +33 562-71-89-33

E-mail: info@invivogen.com

Website: www.invivogen.com



3950 Sorrento Valley Blvd Suite 100
San Diego, CA 92121 - USA

FIG. 92b

Initial Culture Procedure

The first propagation of cells should be for generating stocks for future use. This ensures the stability and performance of the cells for subsequent experiments.

1- Thaw the vial by gentle agitation in a 37°C water bath. To reduce the possibility of contamination, keep the O-ring and cap out of the water. Thawing should be rapid.

2- Remove the vial from the water bath as soon as the contents are thawed, and decontaminate by dipping in or spraying with 70% (v/v) ethanol.

Note: All steps from this point should be carried out under strict aseptic conditions.

3- Transfer cells into a larger vial containing 15 ml of pre-warmed Growth Medium. **Do not add selective antibiotics until the cells have been passaged twice.**

4- Centrifuge vial at 1000-1200 RPM (RCF 200-300 g) for 5 minutes.

5- Remove supernatant containing the cryoprotective agent and resuspend cells with 1 ml of Growth Medium without selective antibiotics.

6- Transfer the vial contents to a 25 cm² tissue culture flask containing 5 ml of Growth Medium without selective antibiotics.

7- Place the flask containing HEK-Blue™-hTLR4 Cells at 37°C in 5% CO₂.

Frozen Stock Preparation

1- Resuspend cells at a density of 5-7 x 10⁶ cells/ml in Freezing Medium freshly prepared with cold Growth Medium.

Note: A T-75 culture flask typically yields enough cells for preparing 3-4 frozen vials.

2- Aliquot 1 ml cells into cryogenic vials.

3- Place vials in a freezing container (Nalgene) and store at -80°C overnight.

4- Transfer vials to liquid nitrogen for long term storage.

Note: If properly stored, cells should remain stable for years.

Cell maintenance

1- Maintain and subculture the cells in Growth Medium supplemented with 1X HEK-Blue™ Selection.

2- Renew Growth Medium 2 times a week.

3- Cells should be passaged when a 70-80% confluency is reached. Detach the cells in presence of PBS by tapping the flask or by using a cell scraper. Do not let the cells grow to 100% confluency.

Note: The response of HEK-Blue™-hTLR4 Cells can be altered by the action of trypsin. Do not use trypsin to detach HEK-Blue™-hTLR4 Cells.

TLR4 Stimulation determined using HEK-Blue™ Detection

For real-time detection of SEAP or high-throughput applications we recommend the use of HEK-Blue™ Detection medium (not provided).

1- Add 20 µl of each sample per well of a flat-bottom 96-well plate.

2- Add 20 µl of a positive control (such as LPS-EK Ultrapure, 100 ng/ml) in one well.

3- Add 20 µl of a negative control (such as sterile, endotoxin-free water) in one well.

4- Remove HEK-Blue™-hTLR4 Cells from the incubator and discard Growth Medium. Rinse cells with PBS, add PBS (5-10 ml for a T-75 flask) and place cells at 37°C for 1-2 min, detach the cells by tapping the flask.

Note: Do not add HEK-Blue™ Detection medium at this point in the protocol as it can lead to high background or false positive readings.

5- Count cells.

6- Prepare a cell suspension ~140,000 cells per ml in HEK-Blue™ Detection medium and immediately add 180 µl of the cell suspension (~25,000 cells) per well.

7- Incubate the plate at 37°C in 5% CO₂ for 6-16 h. SEAP can be determined with naked eye or using a spectrophotometer at 620-655 nm.

TLR4 Stimulation determined using QUANTI-Blue™

QUANTI-Blue™ is 10-times more sensitive than HEK-Blue™ Detection medium and can be used to quantify SEAP activity.

Day One:

1 - Add 20 µl of each sample per well of a flat-bottom 96-well plate.

2 - Add 20 µl of a positive control (such as LPS-EK Ultrapure, 100 ng/ml) in one well.

3 - Add 20 µl of a negative control (such as sterile, endotoxin-free water) in one well.

4- Remove HEK-Blue™-hTLR4 Cells from the incubator and discard Growth Medium. Rinse cells with PBS, add PBS (5-10 ml for a T-75 flask) and place cells at 37°C for 1-2 min, detach the cells by tapping the flask.

5- Count cells.

6 - Prepare a cell suspension of HEK-Blue™-hTLR4 Cells at ~140,000 cells per ml in Test Medium which contains 10% (v/v) heat-inactivated fetal bovine serum (FBS).

Note: Some fetal bovine serum (FBS) may contain alkaline phosphatases that can interfere with SEAP quantification. To ensure that these thermosensitive enzymes are inactive, use heat-inactivated FBS (30 min at 56°C). Heat-inactivated FBS is also commercially available.

7 - Add 180 µl of the cell suspension (~25,000 cells) per well.

8 - Incubate the plate at 37°C in a CO₂ incubator for 20-24 h.

Day Two:

1- Prepare QUANTI-Blue™ following the instructions on the pouch.

2- Add 180 µl of resuspended QUANTI-Blue™ per well of a flat-bottom 96-well plate.

3- Add 20 µl of induced HEK-Blue™-hTLR4 Cells supernatant.

4- Incubate the plate at 37°C incubator for 1-3 h.

5- Determine SEAP levels using a spectrophotometer at 620-655 nm.

Specificity of HEK-Blue™-hTLR4 Cells

As HEK293 cells express endogenous levels of TLR3, TLR5 and NOD1, HEK-Blue™-hTLR4 Cells will respond to their cognate ligands, such as poly(I:C), flagellin and iE-DAP, respectively. In order to identify TLR4-specific responses, we recommend to use HEK-Blue™-Null2 Cells as a control cell line. Furthermore, an anti-hTLR4 neutralizing antibody can be used to ensure the specificity of the TLR4 response.

Note: HEK-Blue™-hTLR4 Cells may be stimulated in a TLR4-independent manner as NF-κB/AP-1 can be activated by a wide variety of stimuli (e.g. TNF-α and PMA).

RELATED PRODUCTS

Product	Catalog Code
HEK-Blue™ Null2 Cells	hkb-null2
250X HEK-Blue™ Selection	hb-sel
QUANTI-Blue™ (5 pouches)	rep-qbl
HEK-Blue™ Detection (2 pouches)	hb-detl
Normocin™	ant-nr-1
Anti-hTLR4-IgA (monoclonal)	mab2-hlr4
pAb-hTLR4 (polyclonal)	pab-hlr4
LPS-EK ultrapure (<i>E. coli</i> 0111:B4)	trl-pelps
LPS-EK ultrapure (<i>E. coli</i> K12)	trl-pek-lps
MPLAs (synthetic monophosphoryl lipid A)	trl-mpis

TECHNICAL SUPPORT

Toll free (US): 888-457-5873

Outside US: (+1) 858-457-5873

Europe: +33 562 71 69 38

E-mail: info@invivo-gen.com

Website: www.invivo-gen.com



3950 Sorrento Valley Blvd. Suite 100
San Diego, CA 92121 - USA

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VIABLE GRAM NEGATIVE BACTERIA LACKING OUTER MEMBRANE AGONISTS OF TLR4/MD-2

CROSS REFERENCE

The present application is a non-provisional application claiming priority to U.S. Provisional Patent Application Ser. No. 61/313,562, filed Mar. 12, 2010, the disclosure of which is incorporated in its entirety herein by reference.

FIELD OF THE INVENTION

The present invention is directed to Gram-negative bacteria substantially lacking a ligand that acts as an agonist of TLR4/MD-2. The present invention is also directed to methods of generating such Gram-negative bacteria and uses thereof.

BACKGROUND OF THE INVENTION

Lipopolysaccharide (LPS) is the main outer membrane surface-associated component in Gram-negative bacteria and is associated with an array of pathological and physiological activities in mammalian host immune responses. LPS-mediated toxicity caused by these bacteria is generally due to lipid A, the hydrophobic moiety of LPS, which can function as an agonist of Toll-like receptor 4 (TLR4)/MD-2. Lipid A comprises two glucosamine residues with six acyl chains attached.

Kdo (3-deoxy-D-manno-octulosonate) is considered an essential component of LPS, and it is believed that the minimal LPS structure required for growth of *E. coli* is two Kdo residues attached to lipid A (Kdo₂-lipid A). Biosynthesis of Kdo begins with API (D-arabinose 5-phosphate isomerase), which converts D-ribulose 5-phosphate (Ru5P) into A5P (D-arabinose 5-phosphate). In *E. coli* K-12, there are two API genes, *kdsD* and *gutQ*. Next, A5P is condensed with phosphoenolpyruvate (PEP) to form Kdo 8-phosphate (Kdo8P), which is then hydrolyzed forming Kdo. Kdo is subsequently activated as the sugar nucleotide CMP-Kdo, which is ultimately transferred to lipid IV_A forming Kdo₂-lipid IV_A. The Kdo-dependent acyltransferases LpxL and LpxM transfer laurate and myristate, respectively, to Kdo₂-lipid IV_A to form Kdo₂-lipid A.

The strain *E. coli* K-12 TCM15, which has both API genes (*kdsD* and *gutQ*) deleted and thus lacks Kdo, is not viable unless supplied with exogenous A5P (e.g., see Meredith and Woodard, Identification of GutQ from *Escherichia coli* as a D-arabinose 5-phosphate isomerase, J Bacteriol 187:6936, 2005). The present invention features viable Gram-negative bacteria that substantially lack a ligand that acts as an agonist of TLR4/MD-2. Additional information regarding TLR4/MD-2 may be found at, for example, Qureshi et al., J. Exp. Med., Vol. 189, No. 4, Feb. 15, 1999, Pages 615-625; Shimazu et al., J. Exp. Med., Volume 189, Number 11, Jun. 7, 1999, Pages 1777-1782; Poltorak et al., Science 282, 2085 (1998), the disclosures of which are incorporated in their entirety by reference herein to the extent that the disclosures are consistent with the present invention. The ligand, for example, may comprise lipid A or a 6-acyl lipid. The viable Gram-negative bacteria comprise suppressor mutations, which enable viability despite lacking otherwise essential Kdo. Mamat et al. have described suppressor mutations in the *yhjD* and *msbA* genes non-conditional of *E. coli* TCM15 derivatives (see Mol Microbiol 67(3):633, 2008).

Any feature or combination of features described herein are included within the scope of the present invention pro-

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vided that the features included in any such combination are not mutually inconsistent as will be apparent from the context, this specification, and the knowledge of one of ordinary skill in the art. Additional advantages and aspects of the present invention are apparent in the following detailed description and claims.

SUMMARY

The present invention features viable Gram-negative bacteria comprising an outer membrane that substantially lacks a ligand (e.g., lipid A, 6-acyl lipopolysaccharide, etc.) that acts as an agonist of TLR4/MD2, especially that lacks an agonist of human TLR4/MD2. The ligand may activate a production of costimulatory immune response molecules in a mammal (e.g., inducing macrophages to synthesize mediators of inflammation). In some embodiments, the Gram-negative bacterium is an *Escherichia coli* strain (e.g., KPM22, KPM22 L1, KPM22 L11, KPM22 L13, KPM22 L14, KPM22 L15, KPM22 L18, KPM22 L20, KPM316, KPM318, KPM334 through KPM362) or a *Pseudomonas* strain.

The viable Gram-negative bacterium may further comprise reduced activity of functional arabinose-5-phosphate (A5P) isomerases KdsD and GutQ. In some embodiments, the remaining activity of the arabinose-5-phosphate isomerases with reduced activity is insufficient to provide substrate for the Kdo biosynthetic pathway (e.g., zero or inadequate substrate for the Kdo biosynthetic pathway as would be understood by one of ordinary skill). In some embodiments, this is achieved by complete deletion of both genes. In the present KPM318 and some earlier *lpxL* *lpxM* deletions allow full restoration of Kdo synthesis (by growing on A5P) while limiting the lipid form to lipid IVA, when grown in the presence of A5P as supplement.

In some embodiments, the viable Gram-negative bacterium further comprises one or more suppressor mutations, for example a suppressor mutation in a transporter (e.g., *MsbA* such as *MsbA*-P50S, *MsbA*-P18S, *MsbA*-T283A, *MsbA*-R310S, or *MsbA*-L48F) thereby increasing the transporter's capacity to transport lipid IV_A, a suppressor mutation affecting membrane protein *YhjD* (e.g., *YhjD*-R134C), a suppressor mutation that enables growth at 42 degrees Celsius, etc.

In some embodiments, one or more genes (e.g., *lpxL*, *lpxM*, *pagP*, *lpxP*, and/or *eptA*) are substantially deleted and/or one or more enzymes (e.g., *LpxL*, *LpxM*, *PagP*, *LpxP*, and/or *EptA*) are substantially inactive. For example, the viable Gram-negative bacterium may comprise a site-specific recombinase scar sequence at a site of a partial or complete deletion of one or more of genes (e.g., *lpxL*, *lpxM*, *pagP*, *lpxP*, *eptA*). *E. coli* strains may include but are not limited to: KPM279, KPM280, KPM288, KPM290, KPM296, KPM300, KPM303, KPM310, KPM312, KPM314, KPM316, KPM317, KPM318, KPM334 through KPM362. In some embodiments, a gene encoding for a DNA restriction enzyme and/or a DNA methylation enzyme and/or a gene encoding for *recA* and/or *endA* is mutated or deleted.

The bacterium may exhibit various growth characteristics. For example, in some embodiments, the bacterium can grow exponentially at 42 degrees Celsius. For example, in some embodiments, the bacterium exhibits an exponential phase doubling time of less than about 35 minutes, less than about 40 minutes, or less than about 45 minutes at above 37 degrees Celsius. In some embodiments, the bacterium remains viable in a salt concentration between about 0.1M and 0.9M.

In some embodiments, the bacterium comprises a means of conferring resistance to an antibiotic. In some embodiments, the bacterium comprises an F plasmid, an F' plasmid, or a

gene encoding for F pilus production. In some embodiments, the bacterium can propagate bacteriophages fd, M13, or bacteriophages related to fd or M13. In some embodiments, the bacterium is competent to take up extracellular DNA (e.g., electrocompetent).

The present invention also features outer membranes derived from such Gram-negative bacteria, the outer membranes substantially lacking a ligand that is an agonist of TLR4/MD2. For example, the outer membrane may be derived from the Gram-negative bacteria described herein. The present invention also features viable Gram-negative bacteria (e.g., Gram-negative bacteria described herein such as *E. coli* and/or *Pseudomonas*) lacking an O-acyl transferase that can acylate a lipid A precursor lipidA or Lipid IV_A. O-acyl transferases may include LpxL, LpxM, LpxP, and PagP.

In some embodiments, a Gram-negative bacterium as described herein is a donor bacterium. For example, the Gram-negative donor bacterium may comprise a DNA cassette comprising a gene (e.g., lpxL, lpxM, pagP, lpxP, eptA) having an open reading frame deletion and a means of conferring resistance to an antibiotic (e.g., kanamycin, penicillin, neomycin, tetracycline, chloramphenicol, or ampicillin), wherein the cassette is flanked by sites that are a target for a site-specific recombinase enzyme.

The present invention also features methods of selecting Gram-negative bacteria capable of exponential growth at a temperature above 40 degrees Celsius, wherein the Gram-negative bacterium substantially lacks a ligand that acts as an agonist of TLR4/MD2. In some embodiments, the method comprises growing a strain that substantially lacks the ligand that acts as an agonist of the TLR4/MD2 receptor and has a suppressor mutation that allows growth between about 30 to 40 degrees Celsius (e.g., a strain described herein); plating the strain on a suitable nutrient medium; and incubating the plated strain at 42 degrees Celsius until single colonies of bacteria appear.

The present invention also features methods of constructing a bacterium substantially lacking a gene such as lpxL, lpxM, pagP, lpxP, and eptA. The method comprises obtaining a viable Gram-negative bacterium comprising an outer membrane that substantially lacks a ligand that acts as an agonist of a TLR4/MD2 receptor (e.g., a strain described herein). In some embodiments, the viable Gram-negative bacterium comprises a DNA cassette comprising a modified gene (e.g., a modified antibiotic resistance gene), wherein the modified gene is a modified target gene having an open reading frame deletion. The DNA cassette may further comprise a means of conferring resistance to an antibiotic and/or may be flanked by appropriate target sites for a site-specific recombinase. The method further comprises subjecting the bacterium to P1 vir transduction and replacing the target gene with the modified gene (e.g., a modified antibiotic resistance gene) via homologous recombination. In some embodiments, the method further comprises deleting the antibiotic resistance gene by transient introduction of a site-specific recombinase capable of acting on sequences that flank the antibiotic resistance gene, thereby deleting the resistance gene and leaving a scar characteristic of the site-specific recombinase.

The present invention also features methods of producing a DNA sample and/or a protein sample substantially free of a ligand that acts as an agonist of TLR4/MD2. The method comprises obtaining a Gram-negative bacterium comprising an outer membrane that substantially lacks the ligand that acts as an agonist of the TLR4/MD2 receptor (e.g., a strain described herein), wherein the bacterium is competent to take up extracellular DNA. For producing the DNA sample, the

method further comprises introducing a DNA vector to the bacterium, wherein the bacterium amplifies the DNA vector, and harvesting a DNA sample from the bacterium via a standard DNA isolation protocol. Such DNA isolation protocols are well known to one of ordinary skill in the art.

For producing the protein sample, the method may comprise introducing a DNA vector expression construct to the bacterium, wherein the vector comprises both a gene encoding a protein of interest expressed from a functional promoter and a selectable marker gene, growing the bacterium and allowing or inducing the bacterium to express the protein of interest, and harvesting the bacterium and treating the bacterium to release the protein of interest. In some embodiments, the bacterium comprises a mutation or deletion in one or more genes such as lola, lolB and/or lpp. In some embodiments, for producing the protein sample, the method may comprise introducing a DNA vector expression construct to the bacterium, wherein the vector comprises both a gene encoding a protein of interest expressed from a functional promoter and a selectable marker gene, growing the bacterium and allowing or inducing the bacterium to express the protein of interest, and removing the bacterium from the culture medium to leave the protein of interest in the culture medium.

The present invention also features a library of bacteria substantially free of a ligand that acts as an agonist of the TLR4/MD2 receptor (e.g., a strain described herein), wherein the library of bacteria expresses a series of variants of a protein. The library of bacteria may be useful for screening the protein variants for activity in a mammalian cell based assay. In some embodiments, the members of the library are generated by phage display or by mutagenesis of a plasmid vector expressing a prototype member of the library.

Preferably, the bacteria are able to grow at least as rapidly in rich media supplemented with arabinose-5-phosphate as they grow in the same rich media lacking arabinose-5-phosphate, allowing a choice of outer membrane composition dependent upon the arabinose-5-phosphate without the supplement leading to a slower growth rate. Growth with supplement should be at least 95% of the unsupplemented growth rate and preferably a faster rate than the unsupplemented rate.

The viable Gram-negative bacteria described herein, various components thereof, reagents, and/or materials, may be available in the form of a kit. For example, in some embodiments, the kit comprises a viable Gram-negative bacterium having an outer membrane substantially free of a ligand that acts as an agonist of TLR4/MD2 (e.g., a strain described herein), wherein the bacterium is competent to take up extracellular DNA.

DEFINITIONS

The term "viable non-toxic Gram-negative bacteria" refers to viable Gram-negative bacterial strains comprising an outer membrane substantially free of a ligand that acts as an agonist of TLR4/MD2.

The terms "cells" and "host cells" and "recombinant host cells", which are used interchangeably herein, refer to cells that are capable of or have been transformed with a vector, typically an expression vector. The host cells used herein may be Gram-negative bacteria. It is understood that such terms refer not only to the particular subject cell, but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

The terms “media” and “culture medium” is recognized in the art, and refers generally to any substance or preparation used for the cultivation of living cells.

The term “derived from,” as used, for example, in the context of deriving lipid IV_A from a strain of Gram-negative bacteria, refers to lipid IV_A that can be obtained from the bacteria or the protein, and is intended to include fragments or portions of proteins.

The term “defective”, as used herein, with regard to a gene or gene expression, may mean that the gene is not a wild type gene and that the organism does not have a wild type genotype and/or a wild type phenotype. The defective gene, genotype or phenotype may be the consequence of a mutation in that gene, or of a gene that regulates the expression of that gene (e.g., transcriptional or post-transcriptional), such that its normal expression is disrupted or extinguished. “Disrupted gene expression” is intended to include both complete inhibition and decreased gene expression (e.g., as in a leaky mutation), below wild type gene expression.

The term “Gram-negative bacteria” is recognized in the art, and refers generally to bacteria that do not retain Gram stain (e.g., the deposition of a colored complex between crystal violet and iodine). In an exemplary Gram stain, cells are first fixed to a slide by heat and stained with a basic dye (e.g., crystal violet), which is taken up by all bacteria (i.e., both Gram-negative and Gram-positive). The slides are then treated with an iodine-KI mixture to fix the stain, washed with acetone or alcohol, and finally counterstained with a paler dye of different color (e.g., safranin). Gram-positive organisms retain the initial violet stain, while Gram-negative organisms are decolorized by the organic solvent and hence show the counterstain. Gram-negative bacteria and cell lines include, but are not limited to, *Escherichia* spp., *Shigella* spp., *Salmonella* spp., *Campylobacter* spp., *Neisseria* spp., *Haemophilus* spp., *Aeromonas* spp., *Francisella* spp., *Yersinia* spp., *Klebsiella* spp., *Bordetella* spp., *Legionella* spp., *Citrobacter* spp., *Chlamydia* spp., *Brucella* spp., *Pseudomonas* spp., *Helicobacter* spp. and *Vibrio* spp.

The term “mutant Gram-negative bacteria”, “LPS mutant Gram-negative bacteria”, “kdsD and gutQ mutant Gram-negative bacteria”, “API mutant Gram-negative bacteria” or similar terms, as used herein, includes Gram-negative bacteria of the invention that have been mutated one or more times in, for example, one or more of the gutQ, kdsD, kdsA, kdsB, waaA, msbA, yhjD genes, of any other biosynthetic, processing, or trafficking gene thereby producing an outer membrane substantially lacking LPS or other ligand that acts as an agonist of TLR4/MD2.

An “immunogenic portion of a molecule”, refers to a portion of the molecule that is capable of eliciting an immune reaction against the molecule in a subject.

The term “isolated” as applied to LPS or lipid IV_A molecules, refers to LPS or lipid IV_A which has been isolated (e.g., partial or complete isolation) from other bacterial components, in particular from the outer membrane.

As used herein, the term “portion” when used in reference to a sequence (e.g., an amino acid sequence of a protein, a nucleic acid sequence of a gene) represents any amount of the referenced sequence (e.g., 0.001%, 0.1%, 1%, 10%, 30%, 50%, 75%, 80%, 85%, 90%, 95%, 98%, 99.999% of an amino acid sequence or nucleic acid sequence).

The term “modulation” as used herein refers to both upregulation (i.e., activation or stimulation, e.g., by agonizing or potentiating) and downregulation (i.e., inhibition or suppression, e.g., by antagonizing, decreasing or inhibiting). The term “inducible” refers in particular to gene expression

which is not constitutive but which takes place in response to a stimulus (e.g., temperature, heavy metals or other medium additive).

The term “nucleic acid” refers to polynucleotides or oligonucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs and as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides.

As used herein, the term “transfection” means the introduction of a nucleic acid (e.g., via an expression vector) into a recipient cell by nucleic acid-mediated gene transfer. “Transformation”, as used herein, refers to a process in which a cell’s genotype is changed as a result of the cellular uptake of exogenous DNA or RNA. In an illustrative embodiment, a transformed cell is one that expresses a mutant form of one or more of the kdsD and gutQ genes. A transformed cell can also be one that expresses a nucleic acid that interferes with the expression of a gutQ, kdsD, kdsA, kdsB, waaA, msbA, yhjD gene of any other biosynthetic, processing, or trafficking gene.

As used herein, the term “transgene” means a nucleic acid (e.g., a mutant kdsD, gutQ, kdsA, kdsB, waaA, msbA, yhjD gene of any other biosynthetic, processing, or trafficking gene, or an antisense transcript thereto) that has been introduced into a cell. A transgene could be partly or entirely heterologous, e.g., foreign, to the transgenic animal or cell into which it is introduced, or, can be homologous to an endogenous gene of the organism or—cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal or cell’s genome in such a way as to alter the genome of the cell into which it is inserted. A transgene can also be present in a cell in the form of an episome.

The term “treating” a subject for a condition or disease, as used herein, is intended to encompass curing, as well as ameliorating at least one symptom of the condition or disease.

The term “vector” refers to a nucleic acid molecule, which is capable of transporting another nucleic acid to which it has been linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as “expression vectors.”

The term “expression system” as used herein refers to an expression vector under conditions whereby an mRNA may be transcribed and/or an mRNA may be translated into protein, structural RNA, or other cellular component. The expression system may be an in vitro expression system, which is commercially available or readily made according to art known techniques, or may be an in vivo expression system, such as a eukaryotic or prokaryotic cell containing the expression vector. In general, expression vectors of utility in recombinant DNA techniques are often in the form of “plasmids” which refer generally to circular double stranded DNA loops that, in their vector form, are not bound to the chromosome. In the present specification, “plasmid” and “vector” are used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and are well known in the art or which become known in the art subsequently hereto (e.g., cosmid, phagemid and bacteriophage vectors).

The term “viable” means that the cells are able to grow and divide exponentially for multiple generations in a suitable nutrient medium, including rich media, and that the cells can be stored under typical storage conditions for that cell type and subsequently re-grown.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows growth curves of *E. coli* KPM22 and the KPM22-like strains KPM22 L1, KPM22 L11, KPM22 L13, KPM22 L14, KPM22 L15, KPM22 L18, and KPM22 L20. Generation times were determined in LB medium with shaking at 200 rpm at 37° C. Generation times (under these conditions) were calculated to be as follows: KPM22 40 min, KPM22 L1 37 min, KPM22 L11 39 min, KPM22 L13 59 min, KPM22 L14 44 min, KPM22 L15 40 min, KPM22 L18 36 min, and KPM22 L20 55 min.

FIG. 2 shows growth curves of *E. coli* strain KPM288 (KPM22 L1 Δ IpxL::Km⁺) and strain KPM290 (KPM22 L11 Δ IpxL::Km⁺) in either Luria-Bertani (LB) media at 37° C. or in LB media supplemented with 15 μ M D-arabinose 5-phosphate (A5P) and 10 μ M D-glucose 6-phosphate (G6P) at 37° C. Generation times in LB media were calculated to be as follows: KPM288 45 min, KPM290 43 min. Results from growth in LB media supplemented with A5P and G6P were as follows: KPM288 ceased to grow exponentially after 2-3 generations, KPM290 46 min.

FIG. 3 shows growth curves of *E. coli* strain KPM303 (KPM22 L11 Δ IpxL Δ IpxM) at 37° C. in either LB media, LB media supplemented with 15 μ M A5P and 10 μ M G6P, Super Broth (SB) media (containing 10 g/L NaCl), or SB media (containing 10 g/L NaCl) supplemented with 15 μ M A5P and 10 μ M G6P. SB media did not improve the growth rate of KPM303 as compared to LB media. However, in contrast to the growth in LB medium supplemented with A5P and G6P, KPM303 continued to grow exponentially after 2-3 generations when cultivated in SB supplemented with A5P and G6P.

FIG. 4 shows growth curves of *E. coli* strains KPM303 (KPM22 L11 Δ IpxL Δ IpxM), KPM312 (KPM22 L11 Δ IpxL Δ IpxM Δ pagP), and KPM316 (KPM22 L11 Δ IpxL Δ IpxM Δ pagP Δ IpxP) at 37° C. in either SB media or SB supplemented with 15 μ M A5P and 10 μ M G6P. Generation times in SB media were as follows: KPM303 54 min, KPM312 50 min, KPM316 46 min. Generation times in SB media supplemented with A5P and G6P were as follows: KPM303 39 min, KPM312 42 min, KPM316 42 min.

FIG. 5 shows growth curves of *E. coli* strain KPM316 at 37° C. in either SB medium supplemented with 10 mM MgSO₄ and 2 mM CaCl₂ or SB medium supplemented with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P. KPM316 had a generation time of 51 min in SB with 10 mM MgSO₄ and 2 mM CaCl₂. KPM316 had a generation time of 46 minutes in SB with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P.

FIG. 6 shows growth curves of *E. coli* strains KPM316 and KPM318 grown in either SB or in SB supplemented with 15 μ M A5P, and 10 μ M G6P at 37° C. The doubling times are very similar in the range 39-44 min.

FIG. 7 shows growth curves of *E. coli* strains KPM296-6 and KPM316 at 37° C. in either SB medium supplemented with 10 mM MgSO₄ and 2 mM CaCl₂ or SB medium supplemented with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P. The growth rate of KPM296-6 in SB medium with 10 mM MgSO₄ and 2 mM CaCl₂ was 48 min. In SB with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P the growth rate of KPM296-6 was 42 min.

FIG. 8 Growth curves of a series of independent isolates selected from KPM296 at 42° C. Growth was in SB medium at 42° C. Individual isolates are numbered in the inset and keyed to the symbols used to represent their growth curve. Considerable variation in generation time is seen, but each shows exponential growth,

FIG. 9 Analysis of PCR products produced by primers flanking each gene to confirm deletions of O-acyl transferase genes and deletion of eptA gene in KPM318. The parental strain BW30270 is used as a control beside KPM318 for each gene analysed. Template DNAs and the gene for which the particular PCR primer pairs were designed are indicated. It can be seen in each case that the parental strain BW30270 gives rise to a larger PCR product than that seen for KPM318. Only the scar sequence remains in the place of the whole gene in KPM318.

FIGS. 10A and 10B HEK-Blue™ Assays of strains BW30270, KPM316 and KPM318. (A) Outer membrane preparations of strains, and (B) whole cells. Numbers of cells added to each well (as cfu—colony forming units) or mass of outer membrane preparation are indicated. Reference LPS from *E. coli* K-12 supplied with the assay kit was run in parallel with all experiments and is shown for comparison with the outer membrane data with which it is most directly comparable on a mass-to-mass basis.

FIG. 11 Charge deconvoluted electrospray-ionization Fourier-transformed ion cyclotron (ESI FT-ICR) mass spectra in negative ion mode of LPS molecules isolated from *E. coli* strains KPM316 (A) and KPM318 (B). The mass numbers given refer to the monoisotopic peaks of the neutral molecules. The peak at 1178.66 u is most likely a triacylated degradation product of lipid IV_A (1404.86 u) produced during LPS isolation as it is not consistent with a known pathway intermediate.

FIG. 12a-g The sequence for *Escherichia coli* KPM316 (msbA52 Δ kdsD Δ gutQ Δ IpxL Δ IpxM Δ pagP Δ IpxP). msbA52 replaces the wild type allele of msbA, wherein a C at 965895 is replaced by a T, resulting in a Serine instead of Proline at amino acid 18 in the MsbA protein. The following were deleted from the parental strain: Δ gutQ (FIG. 12b), Δ kdsD (FIG. 12c), Δ IpxL (FIG. 12d), Δ IpxM (FIG. 12e), Δ pagP (FIG. 12f), and Δ IpxP (FIG. 12g).

FIG. 13 Single nucleotide changes are present in KPM316 relative to the parental strain MG1655, in addition to the msbA52 mutation and the deletion/insertion to inactivate LPS synthetic genes. None are known or predicted to result in any distinctive phenotype.

FIG. 14a-h *Escherichia coli* KPM318 (msbA52 Δ kdsD Δ gutQ Δ IpxL Δ IpxM Δ pagP Δ IpxP Δ eptA). msbA52 replaces the wild type allele of msbA, wherein a C at 965895 is replaced by a T, resulting in a Serine instead of Proline at amino acid 18 in the MsbA protein. The following were deleted from the parental strain: Δ gutQ (FIG. 14b), Δ kdsD (FIG. 14c), Δ IpxL (FIG. 14d), Δ IpxM (FIG. 14e), Δ pagP (FIG. 14f), Δ IpxP (FIG. 14g), and Δ eptA (FIG. 14h).

FIG. 15 The BW30270 and KPM318 strains were sequenced at the Scripps Core DNA sequencing facility using Illumina sequencing. All the Single Nucleotide Polymorphisms (SNP) and Deletion/Insertion Polymorphisms (DIP) are indicated. These SNPs and DIPs are assigned based on the comparison of these strains to the Blattners MG1655 strain. Only those detected at 100% of reads are noted. The msbA-P18S suppressor allele in the original KPM22 L11 strain was identified.

FIG. 16 The growth of the four KPM-318 temperature-resistant derivatives; KPM334, KPM335, KPM336, and KPM337 grown in SB medium at 30° C. were assessed.

FIG. 17 The growth of the four KPM-318 temperature-resistant derivatives, KPM334, KPM335, KPM336, and KPM337 grown in SB medium supplemented with A5P/G6P at 30° C. were assessed.

FIG. 18 The growth of the four KPM-318 temperature-resistant derivatives, KPM334, KPM335, KPM336, and KPM337 grown in SB medium at 37° C. were assessed.

FIG. 19 The growth of the four KPM-318 temperature-resistant derivatives, KPM334, KPM335, KPM336, and KPM337 grown in SB medium supplemented with A5P/G6P at 37° C. were assessed.

FIG. 20 The growth of the four KPM-318 temperature-resistant derivatives, KPM334, KPM335, KPM336, and KPM337 grown in SB medium at 42° C. were assessed.

FIG. 21 The growth of the four KPM-318 temperature-resistant derivatives, KPM334, KPM335, KPM336, and KPM337 grown in SB medium supplemented with A5P/G6P at 42° C. were assessed.

FIG. 22a-d The four KPM-318 temperature-resistant derivatives, KPM334, KPM335, KPM336, and KPM337 were sequenced at the Scripps Core DNA sequencing facility using Illumina sequencing. All the Single Nucleotide Polymorphisms (SNP) and Deletion/Insertion Polymorphisms (DIP) are indicated. These SNPs and DIPs are assigned based on the comparison of these strains to the Blattner's MG1655 strain. Only those detected at 100% of reads are noted. The *msbA*-P18S suppressor allele in the original KPM22 L11 strain was identified.

FIG. 23 ESI FT-ICR mass spectrum in negative ion mode of lipid IV_A (1404.86 u) isolated from *E. coli* KPM337 grown at 42° C. in LB medium. Mass numbers given refer to the monoisotopic masses of neutral molecules. The peak corresponding to triacylated lipid Δ (1178.67 u) is likely an artefact produced during lipid IV_A isolation and/or ionization as it is not consistent with a known pathway intermediate.

FIG. 24 ESI FT-ICR mass spectrum in negative ion mode of LPS isolated from *E. coli* KPM334 grown at 42° C. in LB medium supplemented with A5P/G6P. Mass numbers given refer to the monoisotopic masses of neutral molecules.

FIG. 25 ESI FT-ICR mass spectrum in negative ion mode of LPS isolated from *E. coli* KPM335 grown at 42° C. in LB medium supplemented with A5P/G6P. Mass numbers given refer to the monoisotopic masses of neutral molecules.

FIG. 26 ESI FT-ICR mass spectrum in negative ion mode of LPS isolated from *E. coli* KPM337 grown at 42° C. in LB medium supplemented with A5P/G6P. Mass numbers given refer to the monoisotopic masses of neutral molecules.

FIG. 27 ESI FT-ICR mass spectrum in negative ion mode of LPS isolated from *E. coli* KPM318 grown at 37° C. in LB medium supplemented with A5P/G6P (control). Mass numbers given refer to the monoisotopic masses of neutral molecules. Peak assignments are listed in Table 1.

FIG. 28 Detection of LPS in bacterial cell suspensions of KPM316 and KPM318 grown at 37° C. in either LB medium or LB medium supplemented with A5P/G6P. The *E. coli* K-12 wild-type strain BW30270 was used as a control.

FIG. 29 Relative NE-κB induction in HEK-Blue cells caused by LPS/lipid IV_A isolates from *E. coli* strains BW30270, KPM316, KPM318 and KPM334.

FIG. 30 Human TNF-alpha ELISA to determine the antagonistic activity of LPS/lipid IV_A samples isolated from *E. coli* strains KPM316 and KPM318. For details, see the protocol in the text.

FIG. 31 TNF-alpha release in human macrophages caused by LPS/lipid IV_A samples from *E. coli* strains KPM316 and KPM318 in medium containing 4% AB-serum. The S-LPS of *E. coli* K-235 was used as a control.

FIG. 32 TNF-alpha release in human macrophages caused by LPS/lipid IV_A samples from *E. coli* strains KPM316 and KPM318 in serum-free medium. The S-LPS of *E. coli* K-235 was used as a control.

FIG. 33 IL-8 release in HEK293 hTLR4/MD2 #33 cells stimulated with LPS/lipid IV_A samples from *E. coli* strains KPM316 and KPM318. The S-LPS of *E. coli* K-235 was used as a control.

FIG. 34 IL-8 release in HEK293 hTLR2 #2 cells stimulated with LPS/lipid IV_A samples from *E. coli* strains KPM316 and KPM318. The S-LPS of *E. coli* K-235 was used as a control.

FIG. 35 Maps of plasmids pMAL-c2 and pMAL-p2 for cytoplasmic (upper panel) and periplasmic MalE-LacZα expression (lower panel).

FIG. 36 SDS-PAGE analysis of protein extracts (10 μg each) and culture media (10 μl each). The protein extracts were prepared from uninduced cells and cells after an induction time of 3 hr. The culture media were obtained from cells grown under conditions of overnight IPTG induction. The samples were resolved using 10% polyacrylamide gels and stained with Coomassie blue. Molecular Mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 37 SDS-PAGE analysis of protein extracts (10 μg each) and culture media (10 μl each). The protein extracts were prepared from uninduced cells and cells after an induction time of 3 hr. The culture media were obtained from cells grown under conditions of overnight IPTG induction. The samples were resolved using 10% polyacrylamide gels and stained with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 38 SDS-PAGE analysis (upper panel) of protein extracts (8 μg each) and culture media (10 μl each). The protein extracts were prepared from uninduced cells and cells after overnight induction. The culture media were obtained from cells grown under conditions of overnight IPTG induction. The samples were resolved using 10% polyacrylamide gels and stained with Coomassie blue. For the immunoblots (lower panel), 8 μg of each protein extract and 2.5 μl of each culture supernatant were subjected to SDS-PAGE. The blotted membranes were probed with anti-MalE and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of nitroblue tetrazolium (NBT) and 5-bromo-4-chloro-3-indolylphosphate (BCIP) substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 39 SDS-PAGE analysis (upper panel) of protein extracts (8 μg each) and culture media (10 μl each). The protein extracts were prepared from uninduced cells and cells after overnight induction. The culture media were obtained from cells grown under conditions of overnight IPTG induction. The samples were resolved using 10% polyacrylamide gels and stained with Coomassie blue. For the immunoblots (lower panel), 8 μg of each protein extract and 2.5 μl of each culture supernatant were subjected to SDS-PAGE. The blotted membranes were probed with anti-MalE and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of nitroblue tetrazolium (NBT) and 5-bromo-4-chloro-3-indolylphosphate (BCIP) substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 40 Immunoblot analysis of protein extracts (8 μg each) and culture media (2.5 μl each). The protein extracts were prepared from uninduced cells and cells after an induction time of 3 hr. The culture media were from cells grown under conditions of IPTG induction for 3 hr. The samples were resolved using 10% polyacrylamide gels, followed by blotting and probing of the membranes with anti-MalE and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of NBT and BCIP substrate.

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FIG. 41 SDS-PAGE analysis of protein extracts (6 µg each) and culture media (8 µl each) of pMAL-p2 strains. The protein extracts were prepared from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The culture media were from cells after 3 hr, 6 hr, 12 hr and 24 hr of induction. The samples were resolved using 10% polyacrylamide gels and stained with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 42 Immunoblot analysis of protein extracts (6 µg each) and culture media (10 µl each) of pMAL-p2 strains. The protein extracts were prepared from uninduced cells and cells after induction times of 3 h, 6 h, 12 h and 24 h. The culture media were from cells after 3 h, 6 h, 12 h and 24 h of induction. The samples were resolved using 10% polyacrylamide gels, followed by blotting and probing of the membranes with anti-MalE and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of NBT and BCIP substrate.

FIG. 43 Maps of plasmids pJexpress404:51149 and pJexpress404:51150 for cytoplasmic (upper panel) and periplasmic ApoA1 expression (lower panel).

FIG. 44 SDS-PAGE analysis of protein extracts (6 µg each) prepared from strains BW30270/pJexpress404:51149 and KPM318/pJexpress404:51149. The protein extracts were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M. The arrow indicates the ApoA1 protein.

FIG. 45 SDS-PAGE analysis of protein extracts (6 µg each) prepared from strains KPM334/pJexpress404:51149 and KPM335/pJexpress404:51149. The protein extracts were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M. The arrow indicates the ApoA1 protein.

FIG. 46 SDS-PAGE analysis of protein extracts (6 µg each) prepared from strain KPM336/pJexpress404:51149. The protein extracts were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 47 SDS-PAGE analysis of protein extracts (6 µg each) prepared from strains BW30270/pJexpress404:51150 and KPM318/pJexpress404:51150. The protein extracts were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 48 SDS-PAGE analysis of protein extracts (6 µg each) prepared from strains KPM334/pJexpress404:51150 and KPM335/pJexpress404:51150. The protein extracts were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 49 SDS-PAGE analysis of protein extracts (6 µg each) prepared from strain KPM336/pJexpress404:51150. The protein extracts were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained

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with Coomassie blue. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 50 The optical cell density (OD₆₀₀) vs. number of viable cells (cfu/ml) of strain KPM335/pJexpress404:51150 was evaluated during the period of induced ApoA1 expression.

FIG. 51 SDS-PAGE analysis of culture media from strains BW30270/pJexpress404:51150 and KPM318/pJexpress404:51150. The culture media were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. For the amounts of samples loaded, see Tables 7-11.

FIG. 52 SDS-PAGE analysis of culture media from strains KPM334/pJexpress404:51150 and KPM335/pJexpress404:51150. The culture media were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. For the amounts of samples loaded, see Tables 7-11.

FIG. 53 SDS-PAGE analysis of culture media of KPM336/pJexpress404:51150. The culture media were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels and stained with Coomassie blue. For the amounts of samples loaded, see Tables 7-11. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M.

FIG. 54 Immunoblot analysis of protein extracts (3 µg each) of strains BW30270/pJexpress404:51149 and KPM318/pJexpress404:51149. The protein extracts were prepared from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 10% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of NBT and BCIP substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M and labelled after blotting.

FIG. 55 Immunoblot analysis of protein extracts (3 µg each) of strains KPM334/pJexpress404:51149 and KPM335/pJexpress404:51149. The protein extracts were prepared from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 10% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of NBT and BCIP substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M and labelled after blotting.

FIG. 56 Immunoblot analysis of protein extracts (3 µg each) of KPM336/pJexpress404:51149. The protein extracts were prepared from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 10% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of NBT and BCIP substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M and labelled after blotting.

FIG. 57 Immunoblot analysis of protein extracts (3 µg each) of strains BW30270/pJexpress404:51150 and KPM318/pJexpress404:51150. The protein extracts were prepared from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies,

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and developed in the presence of NBT and BCIP substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M and labelled after blotting.

FIG. 58 Immunoblot analysis of protein extracts (3 µg each) of strains KPM334/pJexpress404:51150 and KPM335/pJexpress404:51150. The protein extracts were prepared from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of NBT and BCIP substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M and labelled after blotting.

FIG. 59 Immunoblot analysis of protein extracts (3 µg each) of KPM336/pJexpress404:51150. The protein extracts were prepared from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 h. The samples were resolved using 12% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed in the presence of NBT and BCIP substrate. Molecular mass protein markers (Broad Range-Bio-Rad) were run in lanes M and labelled after blotting.

FIG. 60 Immunoblot analysis of culture media from strains BW30270/pJexpress404:51150 and KPM318/pJexpress404:51150. The culture media were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed overnight in the presence of NBT and BCIP substrate. For the amounts of samples loaded, see Tables 7-11.

FIG. 61 Immunoblot analysis of culture media from strains KPM334/pJexpress404:51150 and KPM335/pJexpress404:51150. The culture media were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed overnight in the presence of NBT and BCIP substrate. For the amounts of samples loaded, see Tables 7-11.

FIG. 62 Immunoblot analysis of culture media of KPM336/pJexpress404:51150. The culture media were obtained from uninduced cells and cells after induction times of 3 hr, 6 hr, 12 hr and 24 hr. The samples were resolved using 12% polyacrylamide gels, followed by blotting and probing of the membranes with Penta-His antibody and alkaline phosphatase-conjugated goat anti-mouse IgG (H+L) antibodies, and developed overnight in the presence of NBT and BCIP substrate. For the amounts of samples loaded, see Tables 7-11.

FIG. 63 Agarose gel electrophoresis of pMAL-c2 plasmids isolated from four randomly selected transformants of *E. coli* strains BW30270/pMAL-c2, KPM318 (LB)/pMAL-c2, and KPM318 (LB A5P/G6P)/pMAL-c2. The samples were subjected to electrophoresis on a 0.8% agarose gel in TBE buffer. Lane 1, pMAL-c2 control; lane 2, BW30270/pMAL-c2 (1); lane 3, BW30270/pMAL-c2 (2); lane 4, BW30270/pMAL-c2 (3); lane 5, BW30270/pMAL-c2 (4); lane 6, KPM318 (LB)/pMAL-c2 (1); lane 7, KPM318 (LB)/pMAL-c2 (2); lane 8, KPM318 (LB)/pMAL-c2 (3); lane 9, KPM318 (LB)/pMAL-c2 (4); lane 10, KPM318 (LB A5P/G6P)/pMAL-c2 (1); lane 11, KPM318 (LB A5P/G6P)/pMAL-c2 (2); lane 12, KPM318

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(LB A5P/G6P)/pMAL-c2 (3); lane 13, KPM318 (LB A5P/G6P)/pMAL-c2 (4); lane M, 1-kb Plus DNA Ladder (Invitrogen).

FIG. 64 Agarose gel electrophoresis of pMAL-c2 and pMAL-p2 plasmids isolated from two randomly selected transformants of *E. coli* strains KPM334/pMAL-c2, KPM334/pMAL-p2, KPM335/pMAL-c2, and KPM335/pMAL-p2. Lane 1, pMAL-c2 control; lane 2, KPM334/pMAL-c2 (1); lane 3, KPM334/pMAL-c2 (2); lane 4, KPM335/pMAL-c2 (1); lane 5, KPM335/pMAL-c2 (2); lane 6, pMAL-p2 control; lane 7, KPM334/pMAL-p2 (1); lane 8, KPM334/pMAL-p2 (2); lane 9, KPM335/pMAL-p2 (1); lane 10, KPM335/pMAL-p2 (2); lanes M, 1-kb Plus DNA Ladder (Invitrogen).

FIG. 65 Agarose gel electrophoresis of PCR products obtained by using the primer pair 5EC1pxPctrl/3EC1pxPctrl to distinguish between the presence of the IpxP wild-type gene and the ΔIpxP knockout mutation in KPM strains. The biomasses of a potential BW30270 (F'121 Tn10) strain (lane 1) and eight tetracycline-resistant KPM318 (F'121 Tn10) transconjugants (lanes 2-9) were used as templates. The 1-kb Plus DNA Ladder (Invitrogen) is shown in lane M.

FIG. 66 Map of the helper plasmid pMAK705 Km^R CATMUT.

FIG. 67 The *E. coli* strains TOP10 and XL1-Blue were transformed with plasmid pMAK705 Km^R CATMUT. The resulting strains TOP10/pMAK705 Km^R CATMUT and XL1-Blue/pMAK705 Km^R CATMUT were streaked on both LB+30 µg/ml kanamycin and LB+30 µg/ml kanamycin+15 µg/ml chloramphenicol plates.

FIG. 68 shows TABLE 1, which provides examples of *E. coli* strains constructed.

FIG. 69 shows TABLE 2, which lists the peak list of glycoforms detected in *E. coli* KPM318 using ESI FT-ICR MS (FIG. 27).

FIG. 70 shows TABLE 3, which provides the optical density and cell number of the bacterial suspensions immediately prior to induction with IPTG.

FIG. 71 shows TABLE 4, which provides the optical density and cell number of the bacterial suspensions after 3 hr of IPTG induction.

FIG. 72 shows TABLE 5, which provides the optical density and cell number of the bacterial suspensions after 6 hr of IPTG induction.

FIG. 73 shows TABLE 6, which provides the optical density and cell number of the bacterial suspensions after 12 hr of IPTG induction.

FIG. 74 shows TABLE 7, which provides the optical density and cell number of the bacterial suspensions after 24 hr of IPTG induction.

FIG. 75 shows TABLE 8, which demonstrates the process for determining of the amount of culture media obtained from cells immediately before the induction with IPTG.

FIG. 76 shows TABLE 9, which demonstrates the process for determining the amount of culture media obtained from cells after 3 hr of induction.

FIG. 77 shows TABLE 10, which demonstrates the process for determining the amount of culture media obtained from cells after 6 h of induction.

FIG. 78 shows TABLE 11, which demonstrates the process for determining the amount of culture media obtained from cells after 12 hr of induction.

FIG. 79 shows TABLE 12, which demonstrates the process for determining the amount of culture media obtained from cells after 24 hr of induction.

FIG. 80 shows TABLE 13, which provides the number of competent cells.

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FIG. 81 shows TABLE 14, which provides the transformation efficiencies for *E. coli* strains BW30270, KPM318 (LB) and KPM318 (LB A5P/G6P).

FIG. 82 shows TABLE 15, which provides the transformation efficiencies for *E. coli* strains KPM334, KPM335, KPM336, and KPM337.

FIG. 83 shows TABLE 16, which provides the yields of plasmids pMAL-c2 and pMAL-p2 isolated from *E. coli* strains BW30270, KPM318, KPM334, KPM335, KPM336, and KPM337.

FIG. 84 shows TABLE 17, which describes the calculation for the amount of the recipient (BW30270 and KPM318) to add to 500 μ l of the donor (JC19022 F'121 Tn10).

FIG. 85 shows TABLE 18, which describes the calculation for the amount of the recipient (KPM334, KPM335, KPM336, and KPM337) to add to 500 μ l of the donor (JC19022 F'121 Tn10).

FIG. 86 shows TABLE 19, which provides the optical densities (OD₆₀₀) of the strains immediately prior to the M13KO7 infection.

FIG. 87 shows TABLE 20, which provides the number of kanamycin-resistant colonies following infection of potential F'121 Tn10 transconjugants with M13KO7 helper phage.

FIG. 88 shows TABLE 21, which provides the sequences referred to in this application.

FIGS. 89, 90 and 91 show the construction path for each *E. Coli* strain.

FIGS. 92A and 92B show a protocol for HEK-Blue assays.

DESCRIPTION OF PREFERRED EMBODIMENTS

Lipid A, a component of lipopolysaccharide (LPS) which comprises two glucosamine residues to which six acyl chains are attached, functions as an agonist of Toll-like receptor 4 (TLR4/MD-2). TLR4/MD-2 is present on several immune system cells, for example macrophages, monocytes, and dendritic cells. Activation of TLR4/MD-2 via LPS/Lipid A can lead to activation of costimulatory immune response components and molecules, ultimately causing endotoxicity. For example, when LPS becomes bound to TLR4/MD-2 (in humans), cytokine production can be activated, complement can be activated, and coagulation can be activated. Cytokines may include interleukin IL-1, IL-6, IL-8, tumor necrosis factor (TNF) (e.g., TNF α), and platelet activating factor. Such cytokines can stimulate production of mediators of inflammation and septic shock (e.g., prostaglandins, leukotrienes). Complement C3a and C5a can cause histamine release leading to vasodilation and/or affect neutrophil chemotaxis. Blood-clotting Factor XII can activate several responses resulting in thrombosis, plasmin activation (fibrinolysis, hemorrhaging), and the like.

Gram-negative bacteria normally comprise a majority of 6-acyl LPS in their outer membranes. The present invention features viable Gram-negative bacteria comprising an outer membrane that substantially lacks components (e.g., ligands) that act as agonists of Toll-like receptor 4 (TLR4)/MD-2. The components (e.g., ligands) may comprise lipid A, a 6-acyl lipid (e.g., 6-acyl LPS), the like, or a combination thereof. In contrast to normal LPS (or lipid A, 6-acyl lipid), lipid IV_A, or 4-acyl LPS binds less tightly to human, TLR4/MD-2 and acts as a mild antagonist to TLR-4/MD2 rather than as an agonist. In some embodiments, the ligand substantially lacking in the outer membrane comprises a Lipid IV_A, or derivatives of lipid IV_A.

As used herein, the term "substantially lacks" means that the outer membrane has from about zero of the agonist ligand

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up to a level of such ligand that does not induce a response above about 25% of the maximal signal in the HEK-blue assay when 20 μ g of outer membrane is added to a single assay well. In some embodiments, a HEK-Blue assay that may be used in accordance with the present invention may be obtained from InvivoGen, 3950 Sorrento Valley Blvd., Suite 100, San Diego, Calif. 92121 (USA), catalog #hkb-htlr4, and the assay protocol is submitted in FIG. 92. For example, in some embodiments, outer membrane that substantially lacks a ligand that acts as an agonist of Toll-like receptor 4 (TLR4/MD-2) means that the outer membrane does not have the ligand at all. In some embodiments, the outer membrane may have a low amount of agonist for TLR4/MD-2 present at a level that is below the detection limit in a HEK-blue cell-based assay when tested as a membrane extract at up to 20 μ g per well. The human cell line HEK-blue is engineered to be very sensitive to TLR4/MD-2 signaling, and this assay will give a very strong signal when only 20 μ g of LPS is present per well. In some embodiments, a very low signal (e.g., less than about 25% of the maximal value) is seen even at a level of 20 μ g of outer membrane per well.

The Gram-negative bacteria of the present invention include but are not limited to *Escherichia coli*. For example, distantly related Gram-negative species such as *Pseudomonas* species may also be engineered to grow while lacking TLR4/MD2 agonist as a component of their outer membrane. In some embodiments the *Escherichia coli* strain is K-12, W3110, MG1655, B/r, BL21, O157:h7, 042, 101-1,1180, 1357, 1412, 1520, 1827-70, 2362-75, 3431, 53638, 83972, 929-78, 98NK2, ABU 83972, B, B088, B171, B185, 8354, B646, B7A, C, c7122, CFT073, DH1, DH5a, E110019, E128010, E74/68, E851171, EAEC 042, EPECa11, EPECa12, EPECa14, ETEC, H10407, F11, F18+, FVEEC1302, FVEEC1412, GEMS_EPEC1, HB101, HT115, KO11, LF82, LT-41, LT-62, LT-68, MS107-1, MS119-7, MS124-1, MS 145-7, MS 79-2, MS 85-1, NCTC 86, Nissle 1917, NT:H19, NT:H40, NU14, O103:H2, O103:HNM, O103:K+, O104:H12, O108:H25, O109:H9, O111:H-, O111:H19, O111:H2, O111:H21, O111:NM, O115:H-, O115:HNM, O115:K+, O119:H6, O119:UT, O124:H40, O127a:H6, O127:H6, O128:H2, O131:H25, O136:H-, O139:H28 (strain E24377 Δ /ETEC), O13:H11, O142:H6, O145:H-, O153:H21, O153:H7, O154:H9, O157:12, O157:H-, O157:H12, O157:H43, O157:H45, O157:H7 EDL933, O157:NM, O15:NM, O177:H11, >O17:K52:H18 (strain UMN026/ExPEC), O180:H-, O1:K1/APEC, O26, O26:H-, O26:H11, O26:H11:K60, O26:NM, O41:H-, O45:K1 (strain S88/ExPEC), O51:H-, O55:H51, O55:H6, O55:H7, O5:H-, O6, O63:H6, O63:HNM, O6:K15:H31 (strain 536/UPEC), O7:K1 (strain IAI39/ExPEC), O8 (strain IAI1), O81 (strain ED1a), O84:H-, O86a:H34, O86a:H40, O90:H8, O91:H21, O9:H4 (strain HS), O9:H51, ONT:H-, ONT:H25, OP50, Orough:H12, Orough:H19, Orough:H34, Orough:H37, Orough:H9, OUT:H12, OUT:H45, OUT:H6, OUT:H7, OUT:HNM, OUT:NM, RN587/1, RS218, 55989/EAEC, B/BL21, B/BL21-DE3, SE11, SMS-3-5/SECEC, UTI89/UPEC, TA004, TA155, TX1999, or Vir68.

In some embodiments, the viable Gram-negative bacteria of the present invention have reduced activity of the functional D-arabinose-5-phosphate (A5P) isomerases (APIs) KdsD and GutQ. The reduced activity of functional APIs KdsD and GutQ may be a result of substantial inactivation of the APIs, for example a chemical agent functioning to substantially inactivate the APIs, a dominant negative protein functioning to substantially inactivate the APIs, an antibody of fragment thereof that binds and functions to substantially inactivate the APIs, or the like. In some embodiments, the

reduced activity of functional APIs KdsD and GutQ may be a result of a partial or substantial deletion or a mutation in the genes encoding the APIs (e.g., kdsD, gutQ). The bacteria may include *E. coli* K-12 TCM15, BL21, BL21(DE3), W3110.

Suppressor Mutations

The viable Gram-negative bacteria of the present invention comprise a suppressor mutation that enables growth despite lacking any TLR4 agonists in the membrane. For example, the viable gram-negative bacteria may be derived from *E. coli* K-12 TCM15, which lacks both API genes (thus lacks Kdo) and is not viable unless supplied with exogenous ASP. The viable Gram-negative bacteria may comprise a suppressor mutation that allows the bacteria to be viable despite lacking both API genes (and Kdo). Suppressor mutations may include gain-of-function suppressor mutations as well as loss-of-function suppressor mutations. In some embodiments, the suppressor mutation is a mutation in a gene encoding a transporter or a membrane protein, e.g., the transporter MsbA encoded by *msbA* or the membrane protein YhjD encoded by *yhjD*. The suppressor mutation may provide the transporter or membrane protein an increased capacity to transport lipid IV_A. The suppressor mutation may include an amino acid substitution, for example a mutation at amino acid position 18, or at position 50, or at position 283, or at position 310, or at position 448 in MsbA or a mutation at amino acid position 134 in YhjD. In some embodiments, the suppressor mutation results in up-regulated expression of a transporter (e.g., MsbA), increasing the bacterium's capability of transporting lipid IV_A. The suppressor mutation is not limited to the aforementioned examples. The bacteria may include *E. coli* K-12 KPM22, KPM22 L1, KPM22 L11. In some embodiments, the bacteria include *E. coli* K-12 KPM22 L13, KPM22 L14, KPM22 L15, KPM22 L18, KPM22 L20. In some embodiments, the suppressor alleles of the *E. coli* *msbA* gene may be used in distantly related Gram-negative bacterial species (such as *Pseudomonas*) even though the wild type *E. coli* *msbA* gene itself cannot replace the native *msbA* gene.

Non-Revertable Strains

In wild-type Gram-negative bacteria, the O-acyl transferases LpxL and LpxM add O-linked lipids to Kdo2-Lipid IV_A to form a 6-acyl lipid that functions as an agonist of TLR4/MD-2. In the absence of Kdo, the O-acyl transferases LpxL and LpxM fail to use Lipid IV_A as a substrate and do not add the O-linked lipids. However, it is possible that mutations in *lpxL* (encoding LpxL) or *lpxM* (encoding LpxM) may alter specificity of the enzymes, allowing the transferases to use lipid IV_A as a substrate and thereby generating a 6-acyl lipid that functions as an agonist of TLR4/MD-2. Or, mutations may arise in promoters or regulators of *lpxP* or *pagP*, activating expression of these normally absent or very low abundance transferases. Or, mutations may arise in promoters or regulators of *lpxL* or *lpxM*, which may activate their overexpression.

To help avoid these situations, the bacteria of the present invention may further comprise a deletion (e.g. partial deletion, substantial deletion, etc.) in one or more of the following genes: *lpxL*, *lpxM*, *pagP*, and *lpxP*. Or, in some embodiments, one or more enzymes (e.g., *lpxL*, *lpxM*, *pagP*, *lpxP*) are substantially inactivated in the bacterium: In some embodiments, the gene *eptA* encoding for the lipid A phosphoethanolamine transferase is partially or substantially deleted. In some embodiments, the bacteria is *E. coli* K-12 KPM279 (KPM22 Δ*lpxL*::Km⁺), KPM 280 (KPM22 Δ*lpxM*::Km⁺), KPM 288 (KPM22 L1 Δ*lpxL*::Km⁺), KPM 290 (KPM22 L11 Δ*lpxL*::Km⁺), KPM 296 (KPM22 L11 Δ*lpxL*), KPM 300 (KPM22 L11 Δ*lpxL* Δ*lpxM*::Km⁺), KPM 303 (KPM22 L11 Δ*lpxL* Δ*lpxM*), KPM310 (KPM22 L11 Δ*lpxL* Δ*lpxM* Δ*pagP*),

P::Km⁺), KPM312 (KPM22 L11 Δ*lpxL* Δ*lpxM* Δ*pagP*), KPM314 (KPM22 L11 Δ*lpxL* *lpxM* Δ*pagP* Δ*lpxP*::Km⁺), KPM316 (KPM22 L11 Δ*lpxL* Δ*lpxM* Δ*pagP* Δ*lpxP*), KPM317 (KPM22 L11 Δ*lpxL* Δ*lpxM* Δ*pagP* O*lpxP* Δ*eptA*::Km⁺), or KPM 318 (KPM22 L11 Δ*lpxL* Δ*lpxM* Δ*pagP* Δ*lpxP* Δ*eptA*) or further derivatives of these strains.

Laboratory Tools

The present invention also features laboratory tools, reagents, strains (e.g., base strains, donor strains), and the like, derived from the viable Gram-negative bacteria as described. For example, in some embodiments, the bacteria of the present invention are competent to take up extracellular DNA. In some embodiments, the bacteria are electrocompetent. In some embodiments, the bacteria comprise a means of conferring resistance to an antibiotic (e.g., kanamycin, penicillin, neomycin, ampicillin, etc.). In some embodiments, the bacteria comprise a means to express proteins for high-throughput screening on cells. In some embodiments, the bacteria comprise a means to express recombinant proteins for research and/or therapeutic and/or diagnostic use.

The bacteria may comprise at least one additional suppressor mutation that enables growth above 37 degrees Celsius (e.g., at 42 degrees Celsius). The additional suppressor mutations may for example stabilize the outer membrane of the bacteria or enhance transport of a toxic precursor away from the inner membrane. In some embodiments, bacteria can grow exponentially above 37 degrees Celsius, for example at about 38 degrees Celsius, at about 39 degrees Celsius, at about 40 degrees Celsius, at about 41 degrees Celsius, at about 42 degrees Celsius.

In some embodiments, the bacteria exhibit an exponential phase doubling time of less than about 30 minutes at above 37 degrees Celsius. Or, the bacteria may exhibit an exponential phase doubling time of less than 35 minutes or less than 40 minutes or less than about 45 minutes at above 37 degrees Celsius. In some embodiments, the bacteria exhibit an exponential phase doubling time of less than about 30 minutes (or less than about 35 minutes or less than about 40 minutes or less than about 45 minutes) at above 40 degrees Celsius. In some embodiments, the bacteria exhibit an exponential phase doubling time of less than about 30 minutes (or less than about 35 minutes or less than about 40 minutes or less than about 45 minutes) at 42 degrees Celsius. In some embodiments, the bacterial strain is *E. coli* K-12 KPM296-6.

In some embodiments, additional suppressor mutations may alter (e.g., enhance) the bacteria's ability to grow in various salt concentrations. In some embodiments, the viable gram-negative bacteria are viable in a salt (NaCl) concentration between about 0.1M and 0.9M.

Donor strains may provide the ability to rapidly construct new variant strains. The donor strains may comprise one or more of the aforementioned gene modifications, for example partial or substantial deletions in one of the following genes: *lpxL*, *lpxM*, *lpxP*, *pagG*, *eptA*, *kdsD*, *gutQ*, etc. Each donor deletion construct has a selectable marker gene cassette replacing the deleted DNA sequence, and the cassette is flanked by site-specific deletion sites in such an orientation and arrangement that they may be used subsequently to delete the selectable marker gene cassette when the corresponding recombinase is transiently or temporarily introduced into the strain.

In some embodiments, the bacteria further comprise an F plasmid, an F' plasmid, or genes encoding for F pilus production. In some embodiments, the bacteria can propagate bacteriophages fd, M13, or bacteriophages related to fd or M13. In some embodiments a gene encoding for a DNA restriction enzyme or a DNA methylation enzyme is mutated or deleted.

This may allow for enhanced transformation and/or cloning of unmodified DNA or PCR-amplified DNA. In some embodiments a gene encoding for *recA* or *endA* is mutated, partially deleted, or substantially deleted. Such inactivation or deletion of *recA* results in a host that predominantly produces monomeric plasmid DNAs following transformation with a plasmid. Inactivation of *endA* leads to increased yields of supercoiled DNA of a plasmid introduced into such a strain.

The present invention also features an outer membrane of a Gram-negative bacterium that substantially lacks a ligand that is an agonist of a TLR4/MD2 receptor.

Bacteria of the present invention may be used as donor strains. In some embodiments, the donor strains may comprise an outer membrane that substantially lacks a ligand that acts as an agonist of TLR4/MD2. In some embodiments, the donor strains comprise a DNA cassette comprising a gene having an open reading frame deletion. For example, the gene may be selected from the group consisting of *IpxL*, *IpxM*, *pagP*, *IpxP*, and *eptA*. The DNA cassette may further comprise a means of conferring resistance to an antibiotic and/or a recombinase component.

The bacteria of the present invention may retain “scar” DNA sequences at the site(s) of the engineered gene deletions, particularly in one or more of the genes selected from the group consisting of *kdsD*, *gutQ*, *IpxL*, *IpxM*, *pagP*, *IpxP*, and *eptA*. The “scar” is produced upon deletion of the selectable cassette by site-specific recombination. The recombinase may be one selected from the group consisting of FLP, Cre, *Int/Xis*, *Hin*, *Gin*, or the like. The scar produced may be active for subsequent recombination by the same recombinase, or alternatively the scar may be inactive for further recombination events by the same recombinase. Deletion of the selectable cassette DNA results in a strain that may be used again as a recipient for subsequent transfer of a further gene deletion using a similar selectable cassette, thereby facilitating the construction of multiple gene deletions in a single strain.

Methods

The present invention also features methods of selecting a Gram-negative bacterium substantially lacking a ligand that acts as an agonist of TLR4/MD2, wherein the bacterium is capable of exponential growth at a temperature above 40 degrees Celsius. In some embodiments, the method comprises growing the bacteria that substantially lack the ligand that acts as an agonist of the TLR4/MD2 receptor (e.g., lipid A, 6-acyl lipid, etc.) and has a suppressor mutation that allows growth between about 30 to 40 degrees Celsius. The bacteria can then be plated on a suitable nutrient medium and incubated at 42 degrees Celsius. Single colonies that appear under such conditions represent the bacterium substantially lacking the ligand that acts as an agonist of TLR4/MD2 and capable of exponential growth at 42 degrees Celsius.

The present invention also features methods of constructing bacteria substantially lacking a gene selected from the group consisting of *IpxL*, *IpxM*, *pagP*, *IpxP*, and *eptA*. The method comprises obtaining a viable Gram-negative bacterium comprising (i) an outer membrane that substantially lacks a ligand that acts as an agonist of TLR4/MD2 and (ii) a DNA cassette comprising a modified gene, the modified gene being a modified target gene having an open reading frame deletion, the DNA cassette further comprising a means of conferring resistance to an antibiotic and further being flanked by appropriate target sites for a site-specific recombinase. The method further comprises subjecting the bacterium to P1vir transduction and replacing the target gene with the modified resistance cassette gene via homologous recom-

bination. Subsequently, a site-directed recombinase enzyme or DNA encoding the enzyme is introduced into the cells and this enzyme acts on the corresponding recognition sites flanking the cassette to catalyze recombination, leaving a scar sequence only in the chromosome (see Example 3 below). Alternatively, the gene deletion cassette described above may be introduced into the chromosome of the strain directly using a PCR-amplified linear form of the cassette via the “red-gam” homologous recombination method (see BMC Molecular Biology 2008, 9:20). As above, the resistance gene is then subsequently deleted using a site-specific recombination step, again leaving a “scar” sequence. P1vir transduction, red-gam recombination using linear DNA, and site-directed recombination are all techniques well known to one of ordinary skill in the art.

Bacteria, for example Gram-negative bacteria such as *E. coli*, are commonly used as expression systems for amplifying DNA or expressing proteins of interest. In some cases, the harvested DNA or protein obtained from the bacteria may be contaminated with components of the bacteria, for example ligands that act as agonists of TLR4/MD-2 (e.g., lipid A, LPS). The contamination can have deleterious effects on further experiments and procedures, such as transient transfection of mammalian host cell lines, treatment of cultured mammalian cells that serve as reporter lines in cell-based screening assay.

The present invention also features methods of producing DNA samples substantially free of a ligand that acts as an agonist of TLR4/MD-2. The method may comprise obtaining gram-negative bacteria comprising an outer membrane that substantially lacks the ligand that acts as an agonist of TLR4/MD-2. The bacteria are generally competent to take up extracellular DNA. A DNA vector can be introduced to the bacteria via standard methods well known to one of ordinary skill in the art. The bacteria function to amplify the DNA vector, and the bacteria can be grown in appropriate media. The amplified DNA sample can be harvested from the bacteria via a standard DNA isolation protocol well known to one of ordinary skill in the art. Because the bacteria used for amplification of the DNA substantially lacks the ligand that acts as an agonist of TLR4/MD-2, the DNA sample also substantially lacks of the ligand. DNA isolated from these bacteria is of particular use for transient transfection of mammalian cells for expression of proteins encoded by the plasmid. LPS from the normal *E. coli* employed as plasmid hosts can adversely affect the productivity and yield of protein from transient transfection procedures.

The present invention also features methods of producing protein samples substantially free of a ligand that acts as an agonist of TLR4/MD2. The method may comprise obtaining Gram-negative bacteria comprising an outer membrane that substantially lacks the ligand that acts as an agonist of TLR4/MD2 (the bacteria are competent to take up extracellular DNA) and introducing a DNA vector expression construct to the bacteria via standard protocols well known to one of ordinary skill in the art. The DNA vector expression construct comprises both a gene encoding a protein of interest expressed from a functional promoter and a selectable marker gene. In some embodiments, the bacteria comprise mutations in or deletions of at least one of the following genes: *lloA*, *lloB* or *lpp*.

The bacteria transformed with the DNA vector expression construct can then be grown (e.g., via standard methods) so as to allow the bacteria to express the protein of interest. In some embodiments, the bacteria are induced to express the protein of interest. The protein of interest can then be harvested from the bacteria via standard methods. In some embodiments, the

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bacteria are removed from the culture medium to leave the protein of interest behind in the medium. Because the bacteria used for protein expression lack the ligand that acts as an agonist of TLR4/MD-2, the protein sample also substantially lacks of the ligand.

Libraries are extremely useful tools for screening various protein variants. The present invention also features a library of bacteria, the bacteria being substantially free of a ligand that acts as an agonist of TLR4/MD2. The library of bacteria may express a series of variants of a protein. In some embodiments, the library of bacteria is used to screen the protein variants for activity in a mammalian cell based assay, however the present invention is not limited to mammalian cell based assays. Members of the library may be generated via phage display, via mutagenesis of a plasmid vector expressing a prototype member of the library, or via other standard methods.

Various reagents, strains, and the like may be provided (or combined with other reagents, strains, and the like) in the form of a kit. For example, the kit may comprise a viable Gram-negative bacterium having an outer membrane substantially free of a ligand that acts as an agonist of TLR4/MD2, wherein the bacterium is competent to take up extracellular DNA.

EXAMPLES

The examples provided below are merely examples to further clarify the present invention, and do not limit the scope of the invention in any way.

Example 1

Determination of Growth Rates

The following examples describe measurements of growth rates of various strains according to the present invention. The present invention is not limited to the following examples. Growth rates of strains can be determined by monitoring the cell densities at 600 nm of exponentially growing cultures. Fresh overnight cultures can be diluted 1:50 in pre-warmed media to continue the growth of the bacteria to the mid-exponential growth phase (OD_{600} of 0.5 to 0.6). Cultures can then be diluted again to an OD_{600} of about 0.005 in pre-warmed media to keep the cells growing exponentially for determination of generation times. Media may comprise Luria-Bertani (LB) media, and may further comprise 10 g/L NaCl. As shown in FIG. 1, KPM22 L1, KPM22 L11, KPM22 L13, KPM22 L18, and KPM22 L20 were grown at 37 degrees Celsius. KPM22 L1, KPM22 L11, and KPM22 L18 all had generation times between about 36 to 44 minutes.

As shown in FIG. 2, *E. coli* strain KPM288 (KPM22 L1 Δ IpxL::Km⁺) and strain KPM290 (KPM22 L11 Δ IpxL::Km⁺) were grown in either Luria-Bertani (LB) media at 37 degrees Celsius or in LB media supplemented with 15 μ M D-arabinose 5-phosphate (A5P) and 10 μ M D-glucose 6-phosphate (G6P) at 37° C. Generation times in LB media were calculated to be as follows: KPM288 45 min, KPM290 43 min. Results from growth in LB media supplemented with A5P and G6P were as follows: KPM288 ceased to grow exponentially after 2-3 generations, KPM290 46 min.

As shown in FIG. 3, *E. coli* strain KPM303 (KPM22 L11 Δ IpxL Δ IpxM) was grown at 37° C. in either LB media, LB media supplemented with 15 μ M A5P and 10 μ M G6P, Super Broth (SB) media (containing 10 g/L NaCl), or SB media (containing 10 g/L NaCl) supplemented with 15 μ M A5P and 10 μ M G6P. SB media did not improve the growth rate of

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KPM303 as compared to LB media. However, in contrast to the growth in LB medium supplemented with A5P and G6P, KPM303 continued to grow exponentially after 2-3 generations when cultivated in SB supplemented with A5P and G6P.

As shown in FIG. 4, *E. coli* strains KPM303 (KPM22 L11 Δ IpxL Δ IpxM), KPM312 (KPM22 L11 Δ IpxL Δ IpxM Δ pagP), and KPM316 (KPM22 L11 Δ IpxL Δ IpxM Δ pagP Δ IpxP) were grown at 37° C. in either SB media or SB supplemented with 15 μ M A5P and 10 μ M G6P. Generation times in SB media were as follows: KPM303 54 min, KPM312 50 min, KPM316 46 min. Generation times in SB media supplemented with A5P and G6P were as follows: KPM303 39 min, KPM312 42 min, KPM316 42 min.

As shown in FIG. 5, *E. coli* strain KPM316 was grown at 37° C. in either SB medium supplemented with 10 mM MgSO₄ and 2 mM CaCl₂ or SB medium supplemented with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P. KPM316 had a generation time of 51 min in SB with 10 mM MgSO₄ and 2 mM CaCl₂. KPM316 had a generation time of 46 minutes in SB with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P.

As shown in FIG. 6, *E. coli* strains KPM316 and KPM318 were grown at 37° C. in either SB medium or SB medium supplemented with 15 μ M A5P, and 10 μ M G6P. KPM316 and KPM318 showed generation times of 39-44 min in these media.

Example 2

Generation of Temperature-Resistant Strains

The following example describes generation of a temperature-resistant derivative of KPM296. The present invention is not limited to the following example. Fresh overnight cultures of KPM296 grown in LB medium at 37° C. can be plated on LB agar plates and incubated at 42° C. Incubation at 42° C. can be continued for several days, for example four to five days. Clones with colony-forming ability at 42° C. may appear (representing 42° C.-resistant derivatives of KPM296). The 42° C.-resistant strains can be confirmed by overnight growth on LB agar plates at 42° C. KPM296-6 is a 42° C.-resistant derivative of KPM296.

As shown in FIG. 7, *E. coli* strains KPM296-6 and KPM316 (KPM22 L11 Δ IpxL Δ IpxM Δ pagP Δ IpxP) were grown at 37° C. in either SB with 10 mM MgSO₄ and 2 mM CaCl₂, or in SB with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P. The growth rate of KPM296-6 in SB medium with 10 mM MgSO₄ and 2 mM CaCl₂ was 48 min. In SB with 10 mM MgSO₄, 2 mM CaCl₂, 15 μ M A5P, and 10 μ M G6P the growth rate of KPM296-6 was 42 min.

As shown in FIG. 8, a series of *E. coli* strains isolated independently from parallel selections at 42° C. from KPM296 were grown at in SB medium at 42° C. Virtually every isolate tested, including KPM296-6, exhibits exponential growth at 42° C., with a wide variation in doubling times. The parental strain, KPM296, was unable to grow at all in LB or in SB medium at 42° C.

KPM316 and KPM318 have also been successfully used to select a series of independent isolates able to grow at 42° C. by this method.

Example 3

Strain Construction

The following example describes construction of various aforementioned strains. The present invention is not limited

to these examples. Kanamycin resistance cassettes targeting the *IpxL*, *IpxM*, *pagP*, *IpxP*, and/or *eptA* genes can be generated in donor strains using the phage λ Red recombinase procedure, and then transferred to a KPM strain by P1vir transduction. Excision of the kanamycin resistance gene can be carried out in the presence of the FLP recombinase, and the temperature-sensitive helper plasmid pCP20 can be removed. P1vir transduction and other such techniques are well known to one of ordinary skill in the art.

For example, the $\Delta IpxL::Km^+$ cassette can be generated in KPM22 to yield strain KPM279 (KPM22 $\mu IpxL::Km^+$). KPM279 can be used as a donor for transfer of the $\Delta IpxL::Km^+$ cassette to KPM22 L1 via P1vir transduction to yield strain KPM288 (KPM22 L1 $\Delta IpxL::Km^+$) or to KPM22 L11 via P1vir transduction to yield strain KPM290 (KPM22 L1 $\Delta IpxL::Km^+$).

Further, strain KPM316 (KPM22 L11 $\Delta IpxL$ $\Delta IpxM$ $\Delta pagP$ $\Delta IpxP$) can be obtained via successive deletions of the acyl transferases (in the following order) using KPM280 (KPM22 $\Delta IpxM::Km^+$), BW30270 $\Delta IpxP::Km^+$, and BW30270 $\Delta pagP::Km^+$ as donor strains of the targeting cassettes, respectively: KPM 290 (KPM22 L11 $\Delta IpxL::Km^+$)>KPM 296 (KPM22 L11 $\Delta IpxL$)>KPM 300 (KPM22 L11 $\Delta IpxL$ $\Delta IpxM::Km^+$)>KPM 303 (KPM22 L11 $\Delta IpxL$ $\Delta IpxM$)>KPM310 (KPM22 L11 $\Delta IpxL$ $\Delta IpxM$ $\Delta pagP::Km^+$)>KPM312 (KPM22 L11 $\Delta IpxL$ $\Delta IpxM$ $\Delta pagP$)>KPM314 (KPM22 L11 $\Delta IpxL$ $\Delta IpxM$ $\Delta pagP$ $\Delta IpxP::Km^+$)>KPM316 (KPM22 L11 $\Delta IpxL$ $\Delta IpxM$ $\Delta pagP$ $\Delta IpxP$).

KPM318 was derived from KPM316 by P1vir transduction of the $\Delta eptA::Km^+$ created by the λ Red recombinase procedure in BW30270 $\Delta eptA::Km^+$ to give KPM317 (KPM316 $\Delta eptA::Km^+$) which was then cured of the *Km* cassette by transient expression of FLP recombinase. PCR amplification using primers that flank each deletion were used to confirm the deletions against control DNA from the parental BW30270 (FIG. 9). In each case the parental strain shows a larger PCR product with the primers that flank the gene deleted in KPM318.

Example 4

Other Reagents and Methods

The following example describes other reagents and methods that may be used in accordance with the present invention. The present invention is not limited to these examples.

The presence of endotoxin (e.g., LPS) can be detected via standard assays. For example, HEK-Blue™ LPS Detection Kits (Invivogen, San Diego, Calif.) may be used. In this assay, HEK-Blue™-4 cells are extremely sensitive to LPS (lipid A), and can be used to detect concentrations of LPS (lipid A) as low as 0.3 ng/mL. The assay can be followed according to the manufacturer's protocol.

Whole cells and also outer membrane extracts of cells were tested in the HEK-Blue™ LPS Detection Kit. Control wild type cells and outer membranes were prepared from the parent BW30270, and these were tested with samples of cells and extracts from KPM316 and KPM318. The results, shown in FIG. 10, demonstrate that the HEK-Blue™ LPS assay is extremely sensitive to LPS endotoxin, responding to as little as 2 pg of LPS. Signals in any of the samples prepared from KPM316 or KPM318 were at essentially background levels, even at 20 micrograms of outer membrane added to an assay, 9 orders of magnitude less potent for TLR4/MD2 signalling. Whole cells of KPM316 or KPM318 were also unable to elicit a significant signal at the highest levels tested, in contrast to

the whole cells of BW30270, which gave significant response at levels 4 orders of magnitude lower.

Analysis of the ESI-Mass spectra of the outer membrane extracts of KPM316 showed the expected prominent masses for lipid IVS and lipid IVS-Ethanolamine (FIG. 11 panel A). ESI-MS of KPM318 outer membranes showed only lipid IVS (FIG. 10 panel A), as expected since the ethanolamine transferase has been deleted from this strain.

P1vir transduction is a standard method used to move genes/alleles from a donor strain to a recipient strain via P1vir, a mutant bacteriophage that enters the lytic phase upon infection. P1 (P1vir) can package approximately 90 kb of DNA, so it is generally used with a selectable marker. To perform such experiments, donor strains (and recipient strains) are cultured. P1vir can then be added to the donor strain culture and monitored until the culture has completely lysed. Lysate is then harvested and added to the culture of recipient cells. Following incubation of the recipient cells with the lysate, the recipient cells are plated on selective media to select for colonies with the selectable marker (and thus the gene of interest).

The complete sequence of the *E. coli* K-12 strain is provided in Blattner F R et al. (Science. 1997 Sep. 5; 277(5331): 1453-62) and Riley M et al. (Nucleic Acids Res. 2006 Jan. 5; 34(1):1-9. Print 2006). The generation of the KPM316 strain is outlined in FIG. 12. *msbA52* replaces the wild type allele of *msbA*, wherein a C at 965895 is replaced by a T, resulting in a Serine instead of Proline at amino acid 18 in the *MsbA* protein (FIG. 12a). The following were deleted from the parental strain: $\Delta gutQ$ (FIG. 12b), $\Delta kdsD$ (FIG. 12c), $\Delta IpxL$ (FIG. 12d), $\Delta IpxM$ (FIG. 12e), $\Delta pagP$ (FIG. 12f), and $\Delta IpxP$ (FIG. 12g). The KPM316 sequence was compared to that of the wild-type strain MG1655 (FIG. 13). The functions of these mutations are unknown.

The generation of the KPM318 strain is outlined in FIG. 14. *msbA52* replaces the wild type allele of *msbA*, wherein a C at 965895 is replaced by a T, resulting in a Serine instead of Proline at amino acid 18 in the *MsbA* protein (FIG. 14a). The following were deleted from the parental strain: $\Delta gutQ$ (FIG. 14b), $\Delta kdsD$ (FIG. 14c), $\Delta IpxL$ (FIG. 14d), $\Delta IpxM$ (FIG. 14e), $\Delta pagP$ (FIG. 14f), $\Delta IpxP$ (FIG. 14g), and $\Delta eptA$ (FIG. 14f). Examples of generated strains are provided in Table 1.

The KPM318 and BW30270 strains were sequenced at the Scripps Core DNA sequencing facility using an Illumina DNA sequencer. The sequences were generated using paired end reads of 40 or 60 bases. DNA samples were prepared from each strain and used to generate end-tagged libraries. Up to six libraries were run per lane, along with a reference lane. The other lanes were used for additional unrelated DNA reads, which served as further internal controls. Single nucleotide polymorphisms (SNPs) refer to all single base changes defined as being 100% mutant by the Scripps analysis programs when compared to the reference genome, the Blattner's MG1655 strain. Deletion/insertion polymorphisms (DIPS) refer to all the deletions or insertions (up to 6 bp) defined by the Scripps analysis programs, again using MG1655 as the reference. Only those detected at 100% of reads are provided. Whole gene deletions were independently confirmed by separate sequence alignments. The KPM318 sequence was compared to that of the wild-type strain BW30270 (FIG. 15). Sequencing identified the *msbA*-P18S suppressor allele, which was previously established to exist in the original KPM strain (FIGS. 14 and 15). All known changes introduced by strain engineering were determined to be present at 100% frequency. This was true for all engineered deletions and point mutations.

Temperature-resistant derivatives of KPM318 were isolated in an attempt to identify more robust strains. Overnight cultures of KPM318 grown in LB medium at 37° C. were plated onto LB-agar plates and incubated at 42° C. Only after continued incubation of the plates at 42° C. for four to five days, a number of clones were obtained that regained their colony-forming ability at the elevated temperature. The 42° C.-resistant phenotype of randomly selected clones was confirmed by overnight growth on LB-agar plates at 42° C. A series of independent, nonclonal 42° C.-resistant derivatives of KPM318 were identified. Among a total of 24 temperature-resistant KPM318 derivatives, the strains KPM318-9, KPM318-10, KPM318-19 and KPM318-23 displayed the best growth characteristics, being capable of exponentially growing at temperatures of 30° C., 37° C. and 42° C. in either SB medium (FIGS. 16, 18, and 20) or under conditions of restored LPS biosynthesis in SB medium supplemented with 15 μ M D-arabinose 5-phosphate (A5P) and 10 μ M D-glucose 6-phosphate (G6P) (FIGS. 17, 19, and 21). Therefore, these temperature-resistant strains exhibit robust growth characteristics over a range of temperatures.

The KPM318-9, KPM318-10, KPM318-19 and KPM318-23 strains were sequenced at the Scripps Core DNA sequencing facility using an Illumina DNA sequencer (FIG. 22). Specific mutations were identified that may account for the viability of the strains at 42° C. Strains KPM318-9 and KPM318-10 express a *frdD61Y* mutation that alters a ribosomal recycling factor (FIGS. 22a and 22b). The KPM318-19 strain has a frameshift mutation in *efp*, which encodes elongation factor P (FIG. 22c). The KPM318-23 strain has a deletion of P146 and L147 in *dcd*, which encodes the deoxycytidine deaminase gene (FIG. 22d). The specific functions of these mutations are unknown.

The LPS/lipid IVA composition of the KPM318-9, KPM318-10, KPM318-19 and KPM318-23 strains was analyzed. The cultures (2.5 L each) were grown at 42° C. to stationary phase in either LB medium or LB medium supplemented with A5P/G6P. The LPS/lipid IV_A was extracted from the dried biomass of each strain using either the original phenol-chloroform-light petroleum (PCP) procedure for those strains grown in LB medium with A5P/G6P or a modified PCP protocol for strains grown in LB-only medium. Then the extracts were subjected to ESI FT-ICR mass spectrometry. The KPM318-23 strain grown in LB medium predominantly expresses lipid IV_A (peak at 1404.86 u) at 42° C. (FIG. 23). When the 42° C.-resistant KPM318 derivatives were grown in LB medium supplemented with A5P/G6P, biosynthesis of the *E. coli* K-12 core oligosaccharide was restored. There was expression of a similar mixture of different glycoforms in all strains, albeit attached to the tetraacylated precursor lipid IV_A (FIGS. 24-26). LPS isolated from the parental strain KPM318 grown at 37° C. in LB medium supplemented with A5P/G6P was used as a control for all these experiments (FIG. 27). A number of the molecular masses of the different glycoforms expressed by KPM318 could be assigned and are provided in Table 2. Taken together, the overall LPS/lipid IV_A composition of the 42° C.-resistant derivatives of KPM318 did not show any peculiarities with respect to the typical heterogeneous oligosaccharide composition of the K-12 core. All outer membrane preparations of these strains showed no lipid A; they only contained lipid IV_A.

The biological activity of both the bacterial cells and the LPS/lipid IV_A isolated from various KPM strains grown in either LB/SB medium or LB/SB medium supplemented with A5P/G6P was examined using the HEK-Blue LPS detection assay (InvivoGen). For preparation of bacterial cells for this detection assay, 1 ml of an overnight culture of each strain

was sedimented by centrifugation and washed in Dulbecco's phosphate buffered saline (DPBS). To kill the bacterial cells, the pellet was subsequently resuspended in 1 ml of a 10 \times conc. penicillin-streptomycin (Pen-Strep) in DPBS solution. The mixture was incubated at room temperature for 2 hr and stored at 4° C. overnight. At the same time, serial dilutions of the overnight cultures were prepared for calculation of cell number (cfu/ml) of the overnight cultures/Pen-Strep killed cells. The Pen-Strep suspensions of the strains were diluted to 10⁸ cfu/ml in 10 \times conc. Pen-Strep in DPBS solution, and serial dilutions of the suspensions were then prepared in 10 \times conc. Pen-Strep in DPBS solution to yield bacterial cell suspensions of 10⁷, 10⁶, 10⁵, 10⁴, 10³, 10² and 10¹ cfu/ml. A typical HEK-Blue LPS detection assay using serial dilutions of bacterial cell suspensions from strains BW30270, KPM316 and KPM318 is shown in FIG. 28. There is little to no LPS activity in the bacterial cell suspensions from the KPM316 and KPM318 strains grown in LB medium, as compared to the control strain BW30270. There is a slight increase in activity for the KPM316 and KPM318 strains grown in media supplemented with A5P/G6P. There is little to no NF κ B activation induced by serial dilutions of the LPS/lipid IV_A samples isolated from the KPM316 and KPM318 strains (FIG. 29).

The biological activity of the LPS/lipid IV_A isolated from the temperature-resistant strain KPM318-9 grown at 42° C. in LB-only medium and LB medium supplemented with A5P/G6P was compared with the ability of LPS/lipid IV_A samples from BW30270, KPM316 and KPM318 to induce NF κ B activation in HEK-Blue cells. Strain BW30270 was grown at 37° C. in LB medium, whereas strains KPM316 and KPM318 were cultivated at 37° C. in either LB medium or LB medium containing A5P/G6P. To examine the potential antagonistic activity of KPM318-9, constant amounts of the LPS/lipid IV_A isolated from KPM318-9 (256 pg) were mixed with decreasing amounts of BW30270-derived LPS. The LPS/lipid IV_A from KPM318-9 is a potent antagonist of LPS activity as demonstrated by the ability of BW30270 to compete with this antagonist when it is present at high concentrations (FIG. 29, lanes 9-12).

A human TNF-alpha ELISA was performed with LPS/lipid IV_A samples isolated from the KPM316 and KPM318 strains grown at 37° C. in either LB medium or LB medium containing A5P/G6P (FIGS. 30-32). The S-LPS isolated from *E. coli* K-235 was used as a positive control. The blood was separated using Biocoll (density: 1.077 g/mL). Mononuclear cells (MNCs) were isolated and washed twice in Hanks and once in VLE RPMI. The monocytes were differentiated into macrophages by incubating them in Teflon bags with M-CSF. The macrophages were harvested after 7 days. The number of cells was determined. Macrophages were seeded into flat-bottom 96 well plates at 1 \times 10⁵ cells/well in VLE RPMI+100 U penicillin+100 μ g/ml streptomycin+2 mM L-glutamine+4% AB-serum (and free of serum). The LPS/lipid IV_A samples were isolated from KPM316 and KPM318 strains and preincubated at 37° C. and 5% CO₂ for 30 min. S-LPS K-235 was added to the samples for 4 hr. Supernatants were removed and stored overnight at 4° C. An ELISA was performed to assess TNF-alpha activity (BD Biosciences #555212). Serial dilutions of the LPS samples in VLE RPMI without AB-serum were prepared. KPM318 LPS LB, KPM316 LPS LB, KPM318 LPS LBAG, and KPM316 LPS LBAG were prepared at 1 mg/ml in 20 mM HEPES, pH 7.0. Then serial dilutions from 100 μ g/mL to 1 ng/mL were prepared. The plates were coated with capture antibody, which was diluted 1:250 in coating buffer (PBS). The plate was agitated overnight and then washed three times with wash

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buffer. The plate was blocked with 180 μ l assay diluent/well and agitated at room temperature for 1 hr. The plate was washed three times with wash buffer.

Samples were diluted in assay diluent and serial dilutions of the standard were prepared as follows:

- 1:212=500 pg/ml
- 1:2=250 pg/ml
- 1:2=125 pg/ml
- 1:2=62.5 pg/ml
- 1:2=31.25 pg/ml
- 1:2=15.6 pg/ml
- 1:2=7.8 pg/ml
- 1:2=3.9 pg/ml

The plates were agitated with standard, samples and blank at room temperature for 2 hr. The plate was washed three times with wash buffer. The detector solution and detection antibody (biotinylated anti-human TNF- α) were added to the plate at 1:1000. The enzyme reagent (streptavidin-horseradish peroxidase conjugate) was added at 1:250. The plate was agitated at room temperature for 1 hr and then washed three times with wash buffer. The plate was agitated in the dark with TMB (1:20) in substrate buffer. The plate was incubated for a minimum of 30 min until the wells turned blue. The reaction was stopped with 50 μ l/well H_2SO_4 . The absorbance was measured at 450 nm. The LPS/lipid IV_A isolated from the positive control K-235 potentially increased TNF- α activity at all concentrations tested (FIG. 30). The LPS/lipid IV_A from the KPM316 and KPM318 strains was able to inhibit the induction of TNF- α by the K-235-derived LPS at all concentrations tested (FIG. 30); therefore, the LPS/lipid IV_A isolated from the KPM316 and KPM318 strains is a potent antagonist of LPS activity. The LPS/lipid IV_A from the KPM316 and KPM318 strains grown in medium containing 4% AB-serum was able to inhibit the release of TNF- α from macrophages (FIG. 31). The LPS/lipid IV_A from the KPM316 and KPM318 strains grown in serum free medium was able to inhibit the release of TNF- α from macrophages (FIG. 32). Therefore, the LPS/lipid IV_A isolated from the KPM316 and KPM318 strains is a potent inhibitor of TNF- α activity.

LPS is known to exert its inflammatory functions via activation of the TLR4 receptor in human cells. The biological activity of the LPS/lipid IV_A from the KPM316 and KPM318 strains was evaluated by assessing the release of IL-8 from HEK293 hTLR4/MD2 #33 (FIG. 33) and HEK293 hTLR4 #2 cells (FIG. 34). hTLR4/MD2 #33 cells respond to LPS binding, generating a signal, while HEK293 hTLR4 #2 cells respond to peptidoglycan, and not to LPS. Therefore, the latter cell line can be used to assess LPS specificity. S-LPS from the K-235 strain was used as a positive control in these assays. The HEK293 hTLR4/MD2 #33 cell medium was DMEM (Biochrom) supplemented with Pen/Strep/Glu and 10% FCS. There were 50,000 HEK293 hTLR4/MD2 #33 cells/well seeded in the wells. The cells were stimulated in the presence of the LPS/lipid IV_A samples for a period of 24 hr, followed by measurement of human IL-8 release (BD Biosciences #555244). The LPS/lipid IV_A from the KPM316 and KPM318 strains was able to block the release of IL-8 from HEK293 hTLR4/MD2 #33 cells (FIG. 33). The LPS/lipid IV_A extracts from the strains were crude extracts as they were able to promote the release of IL-8 from HEK293 hTLR2 #2 cells (FIG. 34). TLR2 is a receptor for peptidoglycan, another bacterial component that can cause cytokine signalling. The abundance of free peptidoglycan is typically far lower than the levels of LPS, so it is usually a minor component. Here it is used to demonstrate that the extracts do indeed contain material derived from the outer membrane-periplasm of the

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cells, since this is where peptidoglycan is located. The HEK cells over expressing TLR4/MD2 (cell line #33) responded to LPS binding, i.e., released IL-8 (FIG. 33), while the HEK cells over expressing TLR2 (cell line #2), which respond to peptidoglycan, do not respond to LPS (FIG. 34). Therefore, this control confirms that something from the outer membrane extracts was indeed added to the assays in both cases.

The ability of the KPM318-9, KPM318-10, KPM318-19 and KPM318-23 strains to overexpress heterologous genes was assessed. The MalE-LacZ α fusion protein was used as a model protein to investigate the capability of these strains to express cytoplasmic and periplasmic variants of the MalE protein in large quantities under standard growth and induction conditions. The BW30270, KPM318, KPM318-9, KPM318-10, KPM318-19 and KPM318-23 strains were transformed each with plasmids pMAL-c2 and pMAL-p2 for cytoplasmic (FIG. 35, upper panel) and periplasmic MalE-LacZ α (FIG. 35, lower panel) expression, respectively. The following strains were obtained:

- BW30270/pMAL-c2 (control)
- KPM318/pMAL-c2
- KPM318-9/pMAL-c2
- KPM318-10/pMAL-c2
- KPM318-19/pMAL-c2
- KPM318-23/pMAL-c2
- BW30270/pMAL-p2 (control)
- KPM318/pMAL-p2
- KPM318-9/pMAL-p2
- KPM318-10/pMAL-p2
- KPM318-19/pMAL-p2
- KPM318-23/pMAL-p2

To induce expression of MalE-LacZ α isopropyl- β -D-thiogalactoside (IPTG) was added to a final concentration of 0.4 mM when the cultures reached the mid-exponential growth phase at an OD_{600} of approximately 0.6. For strains carrying the plasmid pMAL-c2, the cells were harvested prior to induction (uninduced), 3 hr after induction, as well as after overnight induction. For strains with plasmid pMAL-p2, samples were taken from uninduced cells and after induction times of 3 hr, 6 hr, 12 hr, and 24 hr. The ability to secrete the MalE-LacZ α protein into the medium was additionally examined for strains carrying the pMAL-p2 plasmid, with pMAL-c2 strains used as controls. Protein extracts were prepared using the BugBuster reagent according to the manufacturer's recommendations (Novagen). Western blot analyses using a monoclonal antibody against MalE (NEB) were performed to detect MalE-LacZ α expression.

The expression levels of MalE-LacZ α were highest at 3 hr post-induction in pMAL-c2 strains, and at 3 hr and 6 hr post-induction in pMAL-p2 strains (FIGS. 36-42). Expression of MalE-LacZ α was consistently highest in strains KPM318, KPM318-9 and KPM318-10, showing almost identical expression levels to the BW30270 wild-type controls (FIGS. 36-42). As expected, both Coomassie-blue stained polyacrylamide gels and immunoblots did not detect MalE-LacZ α in the culture media of strains carrying the plasmid pMAL-c2 for cytoplasmic expression of the protein (FIGS. 36-42). In contrast, the abundance of the MalE-LacZ α protein in the culture media of pMAL-p2 strains apparently increased with increasing duration of IPTG induction. This did not only apply to all KPM mutants, but also to the BW30270 wild-type strain (FIGS. 36-42). It is unknown whether the presence of MalE-LacZ α in the culture medium is a result of secretion of the protein as a result of a compromised outer membrane in the KPM strains or simply cell lysis due to periplasmic overexpression of the protein under the experimental conditions used in this study. MBP is known to

be highly expressed in *E. coli*. The KPM18 temperature-resistant derivatives exhibited similar levels of protein expression to the wild-type control strain BW30270. These strains secrete or leak MBP more readily than the wild-type strain, which allows the collection of protein in the absence of cell lysis.

The ability of KPM318 and its temperature-resistant derivatives to produce the human ApoA1 protein was investigated. The apoA1 gene optimized for codon usage of *E. coli* was synthesized and cloned under the control of the Tn5 promoter in pJexpress404 by the company DNA 2.0. For periplasmic expression of ApoA1, the gene was fused to the leader sequence of ompA for the major outer membrane protein A of *E. coli*. In addition, both the cytoplasmic and the periplasmic version of the apoA1 gene were C-terminally fused to a 6xHis-tag-coding sequence. The strains were transformed with pJexpress404:51149 and pJexpress404:51150 for cytoplasmic (FIG. 43, upper panel) and periplasmic ApoA1 (FIG. 43, lower panel) expression, respectively. Despite several attempts, the strain KPM318-23 could not be transformed with the pJexpress404:51149 and pJexpress404:51150 expression vectors. The following strains were obtained:

1. BW30270/pJexpress404:51149 (control)
2. KPM318/pJexpress404:51149
3. KPM318-9/pJexpress404:51149
4. KPM318-10/pJexpress404:51149
5. KPM318-19/pJexpress404:51149
6. BW30270/pJexpress404:51150 (control)
7. KPM318/pJexpress404:51150
8. KPM318-9/pJexpress404:51150
9. KPM318-10/pJexpress404:51150
10. KPM318-19/pJexpress404:51150

The cultures were grown overnight at 37° C. in 5 ml of SB medium containing 100 µg/ml ampicillin. The overnight cultures (1:50) were diluted in 40 ml of pre-warmed SB medium containing 100 µg/ml ampicillin. The cultures were grown at 37° C. and agitated at 250 rpm to an OD₆₀₀ of approximately 0.6. The cell number (cfu/ml) for each strain was determined (Table 3). The uninoculated cultures were centrifuged for 10 min at 6,000 rpm (4° C.). A 1 ml aliquot of each pJexpress404:51150-culture supernatant was obtained for further analysis. The 1-ml culture supernatants and cell pellets were frozen and stored at -80° C. IPTG was added to the cultures (at a final concentration of 0.4 mM). The cells were incubated at 37° C. and agitated at 250 rpm for 3 hr. The cell number (cfu/ml) for each strain (Table 4) was evaluated. After the 3 hr induction, 5 ml of each culture was removed:

1. BW30270/pJexpress404:51149—induced (3 hr)
2. KPM318/pJexpress404:51149—induced (3 hr)
3. KPM318-42C 9/pJexpress404:51149—induced (3 hr)
4. KPM318-42C 10/pJexpress404:51149—induced (3 hr)
5. KPM318-42C 19/pJexpress404:51149—induced (3 hr)
6. BW30270/pJexpress404:51150—induced (3 hr)
7. KPM318/pJexpress404:51150—induced (3 hr)
8. KPM318-42C 9/pJexpress404:51150—induced (3 hr)
9. KPM318-42C 10/pJexpress404:51150—induced (3 hr)
10. KPM318-42C 19/pJexpress404:51150—induced (3 hr)

The induced cultures were centrifuged for 10 min at 6,000 rpm (4° C.). A 1 ml aliquot of each pJexpress404:51150-culture supernatant was obtained for further analysis. The 1-ml culture supernatants and cell pellets were stored at -80° C. The induction was continued at 37° C. and 250 rpm. The cell number (cfu/ml) for each culture was determined strain after 6 hr of induction (Table 5). A 3 ml aliquot of each culture was removed after 6 hr of induction:

1. BW30270/pJexpress404:51149—induced (6 hr)
2. KPM318/pJexpress404:51149—induced (6 hr)
3. KPM318-42C 9/pJexpress404:51149—induced (6 hr)
4. KPM318-42C 10/pJexpress404:51149—induced (6 hr)
5. KPM318-42C 19/pJexpress404:51149—induced (6 hr)
6. BW30270/pJexpress404:51150—induced (6 hr)
7. KPM318/pJexpress404:51150—induced (6 hr)
8. KPM318-42C 9/pJexpress404:51150—induced (6 hr)
9. KPM318-42C 10/pJexpress404:51150—induced (6 hr)
10. KPM318-42C 19/pJexpress404:51150—induced (6 hr)

The induced cultures were centrifuged for 10 min at 6,000 rpm (4° C.).

There was a 1 ml aliquot of each pJexpress404:51150 culture supernatant removed for further analysis. The 1-ml culture supernatants and cell pellets were frozen and stored at -80° C. The induction was continued at 37° C. and 250 rpm. The cell number (cfu/ml) was determined for each strain after 12 hr of induction (Table 6). A 2 ml aliquot of each culture was removed after the 12 hr induction:

1. BW30270/pJexpress404:51149—induced (12 hr)
2. KPM318/pJexpress404:51149—induced (12 hr)
3. KPM318-42C 9/pJexpress404:51149—induced (12 hr)
4. KPM318-42C 10/pJexpress404:51149—induced (12 hr)
5. KPM318-42C 19/pJexpress404:51149—induced (12 hr)
6. BW30270/pJexpress404:51150—induced (12 hr)
7. KPM318/pJexpress404:51150—induced (12 hr)
8. KPM318-42C 9/pJexpress404:51150—induced (12 hr)
9. KPM318-42C 10/pJexpress404:51150—induced (12 hr)
10. KPM318-42C 19/pJexpress404:51150—induced (12 hr)

The induced cultures were centrifuged for 10 min at 6,000 rpm (4° C.). There was 1 ml of each pJexpress404:51150-culture supernatant obtained for further analysis. The 1-ml culture supernatants and cell pellets were frozen and stored at -80° C. The induction was continued at 37° C. and 250 rpm. The cell number (cfu/ml) for each strain was determined after 2 hr of induction (Table 7). There was 1 ml of each culture removed after the 24 hr induction:

1. BW30270/pJexpress404:51149—induced (24 hr)
2. KPM318/pJexpress404:51149—induced (24 hr)
3. KPM318-42C 9/pJexpress404:51149—induced (24 hr)
4. KPM318-42C 10/pJexpress404:51149—induced (24 hr)
5. KPM318-42C 19/pJexpress404:51149—induced (24 hr)
6. BW30270/pJexpress404:51150—induced (24 hr)
7. KPM318/pJexpress404:51150—induced (24 hr)
8. KPM318-42C 9/pJexpress404:51150—induced (24 hr)
9. KPM318-42C 10/pJexpress404:51150—induced (24 hr)
10. KPM318-42C 19/pJexpress404:51150—induced (24 hr)

The cultures were induced for 10 min at 6,000 rpm (4° C.). The pJexpress404:51150-culture supernatants were obtained for further analysis. The 1-ml culture supernatants and cell pellets were frozen and stored at -80° C. The uninoculated and induced cells were thawed and all cell pellets were resuspended in 300 µl of 1× BugBuster. There was 3 µl of 20 mg/ml lysozyme solution added to the samples and 0.5 µl of Benzonase. The samples were incubated at room temperature for 20 min with shaking. The samples were centrifuged at 14,000 rpm for 20 min (4° C.). The 1× Bug Buster contains:

1 ml 10x conc. BugBuster
200 μ l 1 M Tris-HCl, pH 7.5 (20 mM Tris-HCl, pH 7.5)
3.5 μ l 2-mercaptoEtOH (5 mM 2-mercaptoEtOH)

Both the cytoplasmic and the periplasmic version of the human ApoA1 protein, as analyzed by 12% SDS-PAGE, were expressed in *E. coli* strains BW30270, KPM318, KPM318-9 and KPM318-10, but not in KPM318-19 (FIGS. 44-49). The apparent relative molecular mass of the 29-kDa band was in accordance with the calculated mass of the protein (29.4 kDa) fused to the C-terminal histidine tag. Strikingly, periplasmically expressed ApoA1 migrated as two bands with apparent relative molecular masses of 29 kDa and 31 kDa, the latter being consistent with the calculated mass of unprocessed ApoA1 of 31.4 kDa (FIGS. 47 and 48). It has been previously shown that ApoA1 is expressed in the cytoplasm of *E. coli* as a mixture of soluble and insoluble protein, which suggests that the supposed unprocessed form of ApoA1 constitutes the insoluble fraction of the protein that is not accessible to transport to its final destination in the periplasm and processing. However, we currently cannot rule out the possibility that the appearance of the slower migrating band is a result of sample preparation at 95° C. for 2 min prior to SDS-PAGE. In any case, the results indicate that the expression rate of ApoA1 in the KPM strains was at least as high as in BW30270, showing a steady level for at least 6 hr.

In contrast to the experiments performed with MalE-LacZ α , the volume of the culture media for SDS-PAGE analyses was adjusted in relation to the optical density (OD₆₀₀) of pJexpress404:51150-carrying cells so that the amount of the culture supernatant loaded onto the polyacrylamide gel came from one and the same OD₆₀₀ value (Tables 8-12). Remarkably enough and as presented for strain KPM318-10/pJexpress404:51150 in FIG. 50, the optical cell densities of all temperature-resistant strains increased while the number of viable cells decreased over the entire period of IPTG induction (Tables 3-7). As shown in FIGS. 51-53, the strains carrying the pJexpress404:51150 plasmid were not capable of secreting ApoA1 into the culture medium. The weakly Coomassie-stained bands rather resembled the protein banding pattern of the cell extracts and, thus, most likely originated from cell lysis. By using immunoblots with a Penta-His antibody (QIAGEN), we could corroborate all findings of SDS-PAGE analyses (FIGS. 54-62). Taken together, our data suggests that the 42° C.-resistant KPM318 derivatives KPM318-9 and KPM318-10 are suitable hosts for protein expression. Optimization of the conditions for bacterial growth, induction and sample preparation should further improve the expression rate and yield of the proteins of interest.

The DNA transformation ability of the cells was assessed. For preparation of electrocompetent cells, the cultures were grown to mid-exponential growth phase (OD₆₀₀=0.5-0.7) at 37° C. with vigorous shaking (220 rpm). The cells were subsequently washed three times with ice-cold water and twice with ice-cold 10% glycerol. Finally, the cell sediments were resuspended in a small volume of ice-cold 10% glycerol, and 50- μ l aliquots were prepared for storage at -80° C. First, we examined the influence of restored K-12 core oligosaccharide biosynthesis on the transformation of KPM318 with pMAL-c2. Strain BW30270 was grown in LB medium as a control, whereas KPM318 was cultivated in LB medium and LB medium containing A5P/G6P. The cells were harvested for preparation of electrocompetent cells when strains BW30270, KPM318 (LB) and KPM318 (LB A5P/G6P) reached an optical density (OD₆₀₀) of 0.621, 0.613, and 0.519, respectively. In order to use one and the same number

of electrocompetent cells for transformation, we determined the colony forming units per milliliter of the competent cells of each strain (Table 13).

The electrocompetent cells of KPM318 (LB) and KPM318 (LB A5P/G6P) were diluted to 7.3×10^8 cfu/ml with ice-cold 10% glycerol (3.65×10^7 cfu/50 μ l) and transformed each with 25 ng of plasmid pMAL-c2 (FIG. 35). The transformation mixtures were serially diluted, plated onto LB agar plates containing 100 μ g/ml ampicillin and incubated at 37° C. The results in Table 14 demonstrate that strains BW30270, KPM318 (LB) and KPM318 (LB A5P/G6P) were transformed with similar efficiencies. The data further shows that KPM318 predominantly expressing lipid IV_a in the outer membrane when grown in LB-only medium (FIG. 11) was not transformed with higher efficiency than BW30270 or KPM318 under conditions of restored core oligosaccharide biosynthesis.

The plasmid pMAL-c2 from four randomly selected transformants of each strain was isolated from 5-ml overnight cultures grown in LB medium containing 100 μ g/ml ampicillin at 37° C. and 200 rpm. The plasmids were isolated using the Wizard Plus Minipreps DNA Purification System (Promega). Samples of 1 μ l were subsequently run on a 0.8% agarose gel in TBE buffer (FIG. 63). The electrophoresis results indicated that the yield of plasmid pMAL-c2 was apparently almost identical for *E. coli* strains BW30270/pMAL-c2, KPM318 (LB)/pMAL-c2, and KPM318 (LB A5P/G6P)/pMAL-c2.

As a next step, the 42° C.-resistant KPM318 derivatives KPM318-9, KPM318-10, KPM318-19 and KPM318-23 were transformed each with plasmids pMAL-c2 and pMAL-p2 (FIG. 35). The cells were grown in SB medium at 37° C. and harvested for preparation of electrocompetent cells when KPM318-9, KPM318-10, KPM318-19 and KPM318-23 reached an optical density (OD₆₀₀) of 0.618, 0.596, 0.491, and 0.702, respectively. The electrocompetent cells were transformed each with 25 ng pMAL-c2 and 25 ng pMAL-p2. Serial dilutions of the transformation mixtures were then plated onto LB agar plates with 100 μ g/ml ampicillin and incubated at 37° C. The transformation efficiencies for the 42° C.-resistant KPM318 strains are summarized in Table 15. While strains KPM318-9, KPM318-10 and KPM318-19 were transformed with high efficiency, the capability of KPM318-23 to uptake plasmids pMAL-c2 and pMAL-p2 was only marginal. In fact, the latter result was consistent with the failure to transform KPM318-23 with plasmids pJexpress404:51149 and pJexpress404:51150.

The plasmids pMAL-c2 and pMAL-p2 were isolated from 5-ml overnight cultures of two randomly selected transformants of KPM318-9/pMAL-c2, KPM318-9/pMAL-p2, KPM318-10/pMAL-c2, and KPM318-10/pMAL-p2, using the Wizard Plus Minipreps DNA Purification System according to the manufacturer's recommendations (Promega). The samples (1 μ l each) were run on a 0.8% agarose gel in TBE buffer (FIG. 64). Finally, the yields of the isolated plasmids were determined for those strains that were subsequently used for the protein expression studies described above (Table 16). Taken together, both the high transformation efficiency and the acceptable yield of plasmid DNA obtained from a standard miniprep culture suggests that KPM318-9 and KPM318-10 are suitable "base strains" for the development of plasmid DNA production strains.

To develop a KPM "base strain" dedicated to screening proteins derived from phage display libraries, the strain should have an Fplasmid to permit infection with M13 phage. We have used the *E. coli* JC19022 (F'121 Tn10) as a donor strain to transfer the F'121 Tn10 plasmid to BW30270,

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KPM318, KPM318-9, KPM318-10, KPM318-19, and KPM318-23 by a tube mating protocol. The cultures were grown overnight in 5 ml of medium at 37° C. with vigorous shaking (220 rpm). LB medium containing 10 µg/ml tetracycline was used for JC19022 (F'121 Tn10), LB medium for BW30270, and LB medium supplemented with A5P/G6P was used for KPM318 and its temperature-resistant derivatives. The following dilutions of the overnight cultures were set-up using the same media as used for overnight growth:

Donor: 25 µl→5 ml

50 µl→5 ml

100 µl→5 ml

200 µl→5 ml

Recipients: 25 µl→5 ml

50 µl→5 ml

100 µl→5 ml

200 µl→5 ml

The samples were vigorously (220 rpm) shaken at 37° C. for approximately 2 to 3 hr. The optical density (OD₆₀₀) of the suspensions (1 ml) was recorded. The optimal OD₆₀₀ range is 0.08 to 0.2; the dilution with the OD₆₀₀ closest to 0.1 should be used if there are options available (this is true for the donor and recipient cultures). In order to remove the tetracycline from the medium of the donor strain, the culture should be centrifuged, and the cell pellet should be resuspended in 4 ml LB medium. A 1:1 ratio of donor:recipient is used for the transfer. The dilution of the donor dilution is determined and multiplied by 500. This value is divided by the OD₆₀₀ of the recipient to obtain the amount of the recipient in µl to add to 500 µl of the donor. The donor culture (500 µl) is incubated with the appropriate amounts of the recipient cultures (Tables 17 and 18). The mating cultures are incubated at 37° C. for 2 hr without agitation. The cultures are then incubated for another 2 hr at 37° C. and agitated at 220 rpm. The samples are vigorously vortexed to disrupt the mating pairs. Dilutions at 10⁻¹, 10⁻², 10⁻³, and 10⁻⁴ in PBS (pre-warmed to room temperature) for each mating were prepared, and 100 µl of each undiluted and diluted mating culture was added to M9 agar plates containing 1 µg/ml thiamine and 10 µg/ml tetracycline. The cultures were incubated at 37° C. The potential transconjugants were streaked onto M9 agar plates containing 1 µg/ml thiamine and 10 µg/ml tetracycline and incubated at 37° C. The tube mating experiments yielded a number of potential transconjugants for all recipient strains. A subset of potential transconjugants was subsequently examined by PCR for the presence of the ΔlpxP knockout mutation to distinguish between false positive clones and tetracycline-resistant KPM strains. As shown in FIG. 65, all tested tetracycline-resistant KPM318 transconjugants contained the ΔlpxP knockout mutation, which indicated the successful transfer of the F'121 Tn10 plasmid to the KPM strain. By using the lpxP PCR, we also could identify several potential F121 TOO transconjugants of KPM318-9, KPM318-10, KPM318-19 and KPM318-23, which contained the required ΔlpxP knockout mutation.

To provide evidence for the presence of the F'121 Tn10 plasmid in KPM318 and its 42° C.-resistant derivatives, as well as to show that the transconjugants are susceptible to M13 infection, the M13KO7 helper phage was used to infect four randomly selected transconjugants of each strain. As M13KO7 contains the origin of replication from P15A and the kanamycin resistance gene from Tn903 both inserted within the M13 origin of replication, the development of kanamycin-resistant clones following infection is an indication for the susceptibility of a given strain to M13KO7. Overnight cultures of *E. coli* JC19022 (F121 Tn10) and BW30270 (F121 Tn10) in LB medium containing 10 µg/ml tetracycline,

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and KPM318 (F121 Tn10) and 42° C.-resistant KPM318 (F'121 Tn10) derivatives in LB medium with 10 µg/ml tetracycline and A5P/G6P were set-up. The BW30270 and KPM318 strains were grown in LB medium and LB medium supplemented with A5P/G6P, respectively, as controls. The cultures were vigorously agitated (220 rpm) at 37° C. The following strains and potential transconjugants were grown:

1. BW30270 (control)

2. KPM318 (control)

3. JC19022 (F'121 Tn10) (control)

4. BW30270 (F121 Tn10)-1

5. BW30270 (F'121 Tn10)-2

6. BW30270 (F'121 Tn10)-3

7. BW30270 (F'121 Tn10)-4

8. KPM318 (F'121 Tn10)-4

9. KPM318 (F'121 Tn10)-6

10. KPM318 (F'21 Tn10)-7

11. KPM318 (F'121 Tn10)-8

12. KPM318-9 (F'121 Tn10)-1

13. KPM318-9 (F'121 Tn10)-2

14. KPM318-9 (F'121 Tn10)-3

15. KPM318-9 (F'121 Tn10)-4

16. KPM318-10 (F121 Tn10)-1

17. KPM318-10 (F'121 Tn10)-3

18. KPM318-10 (F' 121 Tn10)-4

19. KPM318-10 (F121 Tn10)-5

20. KPM318-19 (F121 Tn10)-3

21. KPM318-19 (F' 121 Tn10)-4

22. KPM318-19 (F'121 Tn10)-5

23. KPM318-19 (F121 Tn10)-6

24. KPM318-23 (F'121 Tn10)-1

25. KPM318-23 (F'121 Tn10)-2

26. KPM318-23 (F'121 Tn10)-3

27. KPM318-23 (F'121 Tn10)-5

The overnight cultures of BW30270 and JC19022 (F'121 Tn10) were grown in 3 ml LB medium (1:100), and KPM318 and the potential transconjugants were cultured in 3 ml of LB medium supplemented with A5P/G6P (1:50). The cultures were grown to an early exponential growth phase at 37° C. with vigorous shaking (280 rpm). A 1 ml aliquot was removed for determination of the OD₆₀₀ of the suspension (Table 19)

The M13KO7 infection experiments resulted in kanamycin resistant colonies for all potential transconjugants of KPM318 and its temperature-resistant derivatives (Table 20). Although the number of kanamycin-resistant colonies significantly varied among the strains, the results suggest that: (i) the conjugative transfer of plasmid F'121 Tn10 to the KPM strains was successful, and (ii) the strains became susceptible to M13 infection. This should provide a fundamental basis for the generation of phage display libraries in temperature-resistant KPM318 derivatives.

The supE44 gene from *E. coli* XL1-Blue was transferred to BW30270, KPM318 and its 42° C.-resistant derivatives. To facilitate selection for supE44 in BW30270, KPM318 and its derivatives, the helper plasmid pMAK705 KmR CATMUT was constructed (FIG. 66). First, the kanamycin resistance gene of plasmid pKD4 was amplified using the primers 5BamHIKmR and 3HindIIIKmR, followed by digestion of the PCR product with BamHI and HindIII. Second, the BamHI/HindIII digested PCR product was cloned into the BamHI/HindIII sites of the temperature-sensitive plasmid pMAK705 to yield pMAK705 KmR. Finally, the codon ACC at position 10 was substituted for a TAG (amber) nonsense codon using primers CATamber and CATwtreverse in site-directed mutagenesis with the Change-IT Mutagenesis System (USB).

(SEQ ID 1)
5BamHICKmR: ATATGGATCCTTACATGGCGATAGCTAGACTGG
(SEQ ID 2)
3Hind111KmR: ATATAAGCTTGAAGAACTCCAGCATGAGATCC
CATamber:
(SEQ ID 3)
GAGAAAAAATCACTGGATATACCTAGGTTGATATATCCCAATGGCA
(SEQ ID 4)
CATwtreverse:
CAGTACTGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATC

To verify the introduction of the amber nonsense codon into the cat gene, the *E. coli* strains TOP10 and XL1-Blue were transformed with plasmid pMAK705 KmR CATMUT. The resulting strains TOP10/pMAK705 KmR CATMUT and XL1-Blue/pMAK705 KmR CATMUT were streaked on both LB+30 µg/ml kanamycin and LB+30 µg/ml kanamycin+15 µg/ml chloramphenicol plates (FIG. 67). In contrast to TOP10/pMAK705 KmR CATMUT carrying the wild-type allele of glnV, strain XL1-Blue/pMAK705 KmR CATMUT was capable of growing on LB+30 µg/ml kanamycin+15 µg/ml chloramphenicol plates, indicating the suppression of the nonsense mutation by supE44 (FIG. 67).

Example 5

Construction of the KPM Derived ΔendA ΔrecA Strains

The ΔrecA::KmR strains KPM348, KPM349, KPM350, KPM351 and KPM352, were each derived from the corresponding ΔendA strains to KPM343, KPM344, KPM345, KPM346 and KPM347. Δ as used in this example means deletion. The ΔrecA::KmR targeting cassette was transferred to KPM343, KPM344, KPM345, KPM346 and KPM347 by P1 vir transduction essentially as described for construction of other knockout mutations:

1. The *E. coli* strain BW26547 carrying the ΔrecA::KmR mutation was used as a donor for transduction. The strain was obtained from the *E. coli* Genetic Stock Center.

2. Phage P1 vir was propagated on BW26547 grown at 37° C. in LB medium with 30 µg/ml kanamycin to obtain a ΔrecA::KmR transducing lysate.
3. For transduction, the ΔendA recipient strains KPM343, KPM344, KPM345, KPM346 and KPM347 were grown at 37° C. in LB medium supplemented with A5P/G6P.
4. Transduction was performed according to standard protocols, with selection of potential transductants at 37° on LB-agar plates containing 30 µg/ml kanamycin.
5. The distance between recA and gutQ is only about 6 kb (theoretical co-transduction rate: about 82%), so potential kanamycin-resistant transductants were tested by PCR for the presence of both the ΔrecA::KmR cassette and the deleted gutQ gene in KPM strains.

gutQ control primers:
(SEQ ID NO: 5)
5'gutQctrl1-GTCGATAAGCTGATTACCGACGC
(SEQ ID NO: 6)
3'gutQctrl2-GTGAACTATTTCGTCAGGCACTGG
recA control primers:
(SEQ ID NO: 7)
5'recActrl1-CTACTGCGTATGCATTGCAG
(SEQ ID NO: 8)
3'recActrl1-TCGTAATCTTCTGCCGTAGC.

6. As a result, strains KPM348, KPM349, KPM350, KPM351 and KPM352 containing ΔrecA::KmR and the original gutQ mutation were obtained.
7. The kanamycin resistance gene is removed using transient transformation by pCP20 to obtain strains KPM353, KPM354, KPM355, KPM356, and KPM357.
8. The above recA primers serve for identifying the elimination of the KanR insert in the recA final strains.

Example 6

E. coli Strain Name Designations

Strain	Description
KPM22 L11	(msbA52 ΔkdsD AgutQ)
KPM290	(msbA52 ΔkdsD AgutQ ΔlpxL::Km ⁺)
KPM296	ΔlpxL derivative of KPM22 L11 (msbA52 ΔkdsD AgutQ ΔlpxL)
KPM300	(msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM::Km ⁺)
KPM303	ΔlpxL ΔlpxM derivative of KPM22 L11 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM)
KPM310	(msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP:: Km ⁺)
KPM312	ΔlpxL ΔlpxM ΔpagP derivative of KPM22 L11 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP)
KPM314	(msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP:: Km ⁺)
KPM316	ΔlpxL ΔlpxM ΔpagP ΔlpxP derivative of KPM22 L11 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP)
KPM317	(msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA::Km ⁺)
KPM318	ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA derivative of KPM22 L11 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA)
KPM334	Temperature-resistant KPM318 derivative KPM318-42C 9 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181)
KPM335	Temperature-resistant KPM318 derivative KPM318-42C 10 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181)
KPM336	Temperature-resistant KPM318 derivative KPM318-42C 19 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA efp')
KPM337	Temperature-resistant KPM318 derivative KPM318-42C 23 (msbA52 ΔkdsD AgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA dcd')

-continued

Strain	Description
KPM338	Temperature-resistant KPM334 derivative (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA::Km ⁺)
KPM339	Temperature-resistant KPM335 derivative (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA::Km ⁺)
KPM340	Temperature-resistant KPM336 derivative (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA efp' ΔendA::Km ⁺)
KPM341	Temperature-resistant KPM337 derivative (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA dcd' ΔendA::Km ⁺)
KPM342	(msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA ΔendA::Km ⁺)
KPM343	Temperature-resistant ΔendA derivative of KPM334 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA)
KPM344	Temperature-resistant ΔendA derivative of KPM335 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA)
KPM345	Temperature-resistant ΔendA derivative of KPM336 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA efp' ΔendA)
KPM346	Temperature-resistant ΔendA derivative of KPM337 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA dcd' ΔendA)
KPM347	ΔendA derivative of KPM318 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA ΔendA)
KPM348	Temperature-resistant derivative of KPM343 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA ArecA::Km ⁺)
KPM349	Temperature-resistant derivative of KPM344 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA ArecA::Km ⁺)
KPM350	Temperature-resistant derivative of KPM345 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA efp' ΔendA ArecA::Km ⁺)
KPM351	Temperature-resistant derivative of KPM346 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA dcd' ΔendA ArecA::Km ⁺)
KPM352	(msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA ΔendA ArecA::Km ⁺)
KPM353	Temperature-resistant ΔendA ArecA derivative of KPM334 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA ArecA)
KPM354	Temperature-resistant ΔendA ArecA derivative of KPM335 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181ΔendA ArecA)
KPM355	Temperature-resistant ΔendA ArecA derivative of KPM336 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA efp' ΔendA ArecA)
KPM356	Temperature-resistant ΔendA ArecA derivative of KPM337 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA dcd' ΔendA ArecA)
KPM357	ΔendA ArecA derivative of KPM318 (msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA ΔendA ArecA)
KPM358	Temperature-resistant KPM334 derivative carrying the plasmid F'121 Tn10 [msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181 (F'121 Tn10)]
KPM359	Temperature-resistant KPM335 derivative carrying the plasmid F'121 Tn10 [msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA frr181 (F'121 Tn10)]
KPM360	Temperature-resistant KPM336 derivative carrying the plasmid F'121 Tn10 [msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA efp' (F'121 Tn10)]
KPM361	Temperature-resistant KPM337 derivative carrying the plasmid F'121 Tn10 [msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA dcd' (F'121 Tn10)]
KPM362	KPM318 derivative carrying the plasmid F'121 Tn10 [msbA52 ΔkdsD ΔgutQ ΔlpxL ΔlpxM ΔpagP ΔlpxP ΔeptA (F'121 Tn10)]

The following disclosures of the following patents are incorporated in their entirety by reference herein: WIPO Application No. 2007/084633. References and publications cited herein are incorporated in their entirety by reference herein to the extent that these references are consistent with the present invention.

Various modifications of the invention, in addition to those described herein, will be apparent to those skilled in the art from the foregoing description. Such modifications are also

intended to fall within the scope of the appended claims. Each reference cited in the present application is incorporated herein by reference in its entirety.

Although there has been shown and described the preferred embodiment of the present invention, it will be readily apparent to those skilled in the art that modifications may be made thereto which do not exceed the scope of the appended claims. Therefore, the scope of the invention is only to be limited by the following claims.

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<212> TYPE: DNA

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<212> TYPE: DNA

<213> ORGANISM: *Escherichia coli*

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<212> TYPE: DNA

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<212> TYPE: DNA

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gataccttca tgttatcgct ccttaagcca cttcttgatg atggctttgg taaaacagat 180

cgctccgtgc tgggtgtgat gccgctggcg gtgatcggcg tgatgatttt acgtggtatc 240

accagctatg tctccagcta ctgtatctcc tgggtatcag gaaagggtgt aatgaccatg 300

cgtcgccgcc tgtttgttca catgatggga atgccagttt cattctttga caaacagtca 360

acgggtacgc tgttgtcacg tattacctac gattccgaac aggttgcctc ttcttcttcc 420

ggcgactga ttactgttgt gcgtgaaggt gcgtcgatca tcggcctgtt catcatgatg 480

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gcgattccgc ttgtatcgaa gcgttttcgc aacatcagta aaaacatgca gaacaccatg 600

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What is claimed is:

1. An isolated, viable, non-conditional, Gram-negative mutant bacterium, wherein said bacterium is *Escherichia coli* and comprises an outer membrane that substantially lacks a ligand that acts as an agonist of a human TLR4/MD-2 receptor, said ligand comprising lipid A, wherein the bacterium comprises (a) a mutation in at least one of the genes selected

60 from the group consisting of *kdsA*, *kdsC*, *kdsB*, and *waaA*, or a mutation in each of the *kdsD* and *gutQ* genes, wherein said mutation results in a disruption in the biosynthesis of (Kdo)₂-lipid IV_A, (b) a mutation in each of the genes *pagP* and *eptA* wherein said mutation substantially inactivates the enzymatic activity of each of the proteins encoded by the *pagP* and *eptA* genes, and (c) a suppressor mutation in the

msbA gene resulting in an increased capacity of the encoded MsbA protein to transport lipid IV_A.

2. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, selected from the group consisting of K-12 strains, W3110, MG1655, B/r, BL21, O157:h7, 042, 101-1, 1180, 1357, 1412, 1520, 1827-70, 2362-75, 3431, 53638, 83972, 929-78, 98NK2, ABU 83972, B, B088, B171, B185, B354, B646, B7A, C, c7122, CFT073, DH1, DH5 α , E110019, E128010, E74/68, E851/71, EAEC 042, EPECa11, EPECa12, EPECa14, ETEC, H10407, F11, F18 α , FVEC1302, FVEC1412, GEMS_EPEC1, HB101, HT115, KO11, LF82, LT-41, LT-62, LT-68, MS107-1, MS119-7, MS124-1, MS 145-7, MS 79-2, MS 85-1, NCTC 86, Nissle 1917, NT:H19, NT:H40, NU14, O103:H2, O103:HNm, O103:K+, O104:H12, O108:H25, O109:H9, O111H-, O111:H19, O111:H2, O111:H21, O111:NM, O115:H-, O115:HMN, O115:K+, O119:H6, O119:UT, O124:H40, O127a:H6, O127:H6, O128:H2, O131:H25, O136:H-, O139:H28 (strain E24377A/ETEC), O13:H11, O142:H6, O145:H-, O153:H21, O153:H7, O154:H9, O157:12, O157:H-, O157:H12, O157:H43, O157:H45, O157:H7 EDL933, O157:NM, O15:NM, O177:H11, O17:K52:H18 (strain UMN026/ExPEC), O180:H-, O1:K1/APEC, O26, O26:H-, O26:H11, O26:H11:K60, O26:NM, O41:H-, O45:K1 (strain S88/ExPEC), O51:H-, O55:H51, O55:H6, O55:H7, O5:H-, O6, O63:H6, O63:HNm, O6:K15:H31 (strain 536/UPEC), O7:K1 (strain IAI39/ExPEC), O8 (strain IAI1), O81 (strain ED1a), O84:H-, O86a:H34, O86a:H40, O90:H8, O91:H21, O9:H4 (strain HS), O9:H51, ONT:H-, ONT:H25, OP50, Orough:H12, Orough:H19, Orough:H34, Orough:H37, Orough:H9, OUT:H12, OUT:H45, OUT:H6, OUT:H7, OUT:HNm, OUT:NM, RN587/1, RS218, 55989/EAEC, B/BL21, B/BL21-DE3, SE11, SMS-3-5/SECEC, UTI89/UPEC, TA004, TA155, TX1999, and Vir68.

3. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, further comprising a mutation in the lpxL gene.

4. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, further comprising a mutation in the lpxM gene.

5. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, further comprising a mutation in the lpxP gene.

6. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, further comprising a mutation in each of the lpxL, lpxM, and lpxP genes.

7. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, wherein the kdsD, gutQ, lpxL, lpxM, pagP, lpxP and eptA genes are disrupted in said bacterium.

8. The viable, non-conditional, Gram-negative mutant bacterium of claim 1 or 3, wherein the msbA mutation results in an amino acid substitution selected from the group consisting of MsbA-P18S, MsbA-L48F, MsbA-P50S, MsbA-T283A, and MsbA-R310S.

9. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, wherein the kdsD, gutQ, lpxL, lpxM, pagP, lpxP and eptA genes are disrupted, and wherein the bacterium comprises a mutation in the msbA gene resulting in an amino acid substitution of P18S in the MsbA protein.

10. The viable, non-conditional, Gram-negative mutant bacterium of claim 9, wherein the bacterium further comprises at least one additional mutation to enable growth at 42° C.

11. The viable, non-conditional, Gram-negative mutant bacterium of claim 10, designated KPM335.

12. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, 7 or 9, wherein a gene coding for RecA or EndA is mutated or deleted.

13. The viable, non-conditional, Gram-negative mutant bacterium of claim 12, designated KPM344 or KPM353.

14. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, further comprising an F plasmid, an F' plasmid, or genes encoding for F pilus production.

15. The viable, non-conditional, Gram-negative mutant bacterium of claim 1, wherein the bacterium can propagate bacteriophages fd, M13, or bacteriophages related to fd or M13.

16. The viable, non-conditional, Gram-negative mutant bacterium of claim 14 or 15, designated KPM358.

17. A method of producing a DNA sample substantially free of a ligand that acts as an agonist of TLR4/MD-2, the method comprising:

- (a) obtaining a Gram-negative mutant bacterium according to claim 1;
- (b) introducing a DNA vector to the bacterium, such that the bacterium functions to amplify the DNA vector; and
- (c) harvesting a DNA sample from the bacterium with amplified DNA via a standard DNA isolation protocol.

18. A method of producing a protein sample substantially free of a ligand that acts as an agonist of TLR4/MD-2, the method comprising:

- (a) obtaining a Gram-negative mutant bacterium according to claim 1;
- (b) introducing a DNA vector expression construct to the bacterium, the vector comprising both a gene encoding a protein of interest expressed from a functional promoter and a selectable marker gene;
- (c) growing the bacterium transformed with the DNA vector expression construct;
- (d) allowing or inducing the bacterium transformed with the DNA vector expression construct to express the protein of interest; and
- (e) removing the bacterium to release the protein of interest.

19. The mutant bacterium of claim 1 or 7, further comprising a mutation or deletion in the lpp gene.

20. The mutant bacterium of claim 1 or 7, further comprising a fir-D61Y mutation.

21. The mutant bacterium of claim 1 or 7, wherein said bacterium is competent for transformation.

22. A method of expressing a protein utilizing a viable, non-conditional, Gram-negative mutant bacterium, comprising:

- transfecting the bacterium of claim 1 or 7 with a plasmid containing the nucleotide sequence encoding the protein to be expressed;
- culturing said bacterium in a fermentation medium having a NaCl concentration in the range of 0.1M to 0.9M; and
- expressing the protein in said bacterium in the culture.

23. The mutant bacterium of claim 1, wherein the strain comprises a mutation in each of kdsD and gutQ, wherein said mutation results in inactivation of the encoded D-arabinose-5-phosphate isomerases and a disruption in the biosynthesis of (Kdo)₂-lipid IV_A.

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